

US-10-788- 639 TGGGAAAGTCCAGGAGCTGTTAAGAAAGTTGGATAAGATTCCCTTGCACCTCGCTGCC
US-10-788- 643 TGGGAAAGTCCAGGAGCTGTTAAGAAAGTTGGATAAGATTCCCTTGCACCTCGCTGCC
US-10-788- 675 TGGGAAAGTCCAGGAGCTGTTAAGAAAGTTGGATAAGATTCCCTTGCACCTCGCTGCC
US-10-788- 1038 TGGGAAAGTCCAGGAGCTGTTAAGAAAGTTGGATAAGATTCCCTTGCACCTCGCTGCC
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consensus TGGGAAAGTCCAGGAGCTGTTAAGAAAGTTGGATAAGATTCCCTTGCACCTCGCTGCC
US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 1099 CATCAGAAAGCTGAGGCGTGCCAGAGCACAAAGACTGGGGCAACTGTAGATGTGTTTC
US-10-788- 1099 CATCAGAAAGCTGAGGCGTGCCAGAGCACAAAGACTGGGGCAACTGTAGATGTGTTTC
consensus catcagaaagcctgaggcgtgccagagacacaaagactgggggcaactgtagatgtggtttc
US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 1160 TAGTCTGGCTCGCACTAACTTGCTGTGTAACTTGAACCTGACACAAATTCCTTCGGGA
US-10-788- 1160 TAGTCTGGCTCGCACTAACTTGCTGTGTAACTTGAACCTGACACAAATTCCTTCGGGA
consensus tagtctggcctctgccactaacttgctgtgtaaccttgaactacacaaattctcttcggga
US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 1221 CCTCAATTTCCACTTTGTAAATGAGGGTGGAGGTGGGAATAGGATCTCGAGGAGACTATT
US-10-788- 1221 CCTCAATTTCCACTTTGTAAATGAGGGTGGAGGTGGGAATAGGATCTCGAGGAGACTATT
consensus cctcaatttccactttgtaaaaatgaggggtggaggtgggaataggatctcgaggagactatt
US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 1282 GGCATATGATTCCAAGGACTCCAGTCCCTTTTGAATGGCAGAGCTGAGAGAGAGAGAG
US-10-788- 1282 GGCATATGATTCCAAGGACTCCAGTCCCTTTTGAATGGCAGAGCTGAGAGAGAGAGAG
consensus ggcataatgattccaaggactccagtgccttttgaatggcagaggtgagagagagagagag

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 1343 AAAGAGAGAGAAATGAATGCAGTTGCAATTGATTCAAGGTCACTTCCAGAAATTCAGA
US-10-788- 1343 AAAGAGAGAGAAATGAATGCAGTTGCAATTGATTCAAGGTCACTTCCAGAAATTCAGA
consensus aaagagagagagaatgaatgcagttgcaattgattcagtgccaagggtcacttccagaatttcaga
US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 1404 GTTGTGATGCTCTCTTCTGACAGCCAAAGATGAAAAACAAACAGAAAAAAGTAAAGA
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consensus gttgtgatgctctcttctgacagccaagatgaaaaacaaacagaaaaaagtaaga
US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 1465 CTCATTATTTATGGCTGACATATTTACGGCTGACAAACTCTCTGGAAGAAGCTATGCTGCTTCC
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consensus gtctatttatggctgacataattacggctgacaaactcctggagaagctatgctgcttcc
US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 1526 CAGCTGCGCTTCCCGGATGTTTGGCTACCTCCACCCCTCCATCTCAAGAATAAATCAATCA
US-10-788- 1526 CAGCTGCGCTTCCCGGATGTTTGGCTACCTCCACCCCTCCATCTCAAGAATAAATCAATCA
consensus cagcctggcctccccggatgtttggctacctccaccctccatctctcaagaataaacaatca
US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675
US-10-788- 1587 TCCATTGGGGTAGAAAAAGGAGAGAGGTCCGAGGGTGGTGGGAGGATAGAAATCACATCCGC
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consensus      tccattggggtagaaaaagagaggggtccgaggggtggtgggagggatagaaatcacatccgc
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US-10-788-    643
US-10-788-    675
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consensus      cccaaacttcccaagagcagcatccctcccccagcccatagccatgttttaagtcacctt
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US-10-788-    639
US-10-788-    643
US-10-788-    675
US-10-788- 1709 CCGAAGAGAAAGTGAAGGTTCAAGGACACTGGCCTTGCAAGCCCGAGGAGCAGCCATCAC
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consensus      ccgaagagaagtgaaggttcaaggacactgacctgagggcccgaggagcagccatcac
US-10-788-    533
US-10-788-    639
US-10-788-    643
US-10-788-    675
US-10-788- 1770 AAACTCAGACAGCAGCAGATCCCTTTTGAGACACCGCCTTCTGCCACCACTCACGGACAC
US-10-788- 1770 AAACTCAGACAGCAGCAGATCCCTTTTGAGACACCGCCTTCTGCCACCACTCACGGACAC
consensus      aaactcacagaccagcacatcccttttgagacacgcgccttctgcccaccactcacggacac
US-10-788-    533
US-10-788-    639
US-10-788-    643
US-10-788-    675
US-10-788- 1831 ATTTCGCTAGAAAACAGCTTCTTACTGCTCTTACATGATGGCATATCTTACACTAAA
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consensus      attctgcctagaaaacagcttcttactgctcttacctatcatgtaggcatatcttacactaaa
US-10-788-    533
US-10-788-    639
US-10-788-    643
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US-10-788-    533
US-10-788-    639
US-10-788-    643
US-10-788-    675
US-10-788- 1953 ATAGCTGCCACCCCAAAATCTTTTGAATAATCATTTCCAGACAACCTCTTACTTCTGTGT
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consensus      atagctgccaccaccaaaaatcttttgaataatcatttccagacacaccttacttcttctgtgt
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US-10-788-    643
US-10-788-    675
US-10-788- 2014 AGTTTTTAATTTGTTTAAAAAAAAGTTTAAACAGAGCACATGACATATGAAAAGCTGC
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consensus      agtttttaattgttaaaaaaaagtttttaacagagcacatgacatatgaaagcctgc
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US-10-788- 2075 AGGACTGCTGCTTTTTTTTGGCAATTTCTTCCACGTGGGACTTGTCCACAAGAAATGAAAGTAG
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consensus      aggactggctcggttttttggcaattcttccacgtgggacttgtccacaagaatgaaagtag
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US-10-788-    639
US-10-788-    643
US-10-788-    675
US-10-788- 2136 TGGTTTTTAAAGAGTTAAGTTACATATTTTCTCACTTAAGTTATTTATGCAAAAGTT
US-10-788- 2136 TGGTTTTTAAAGAGTTAAGTTACATATTTTCTCACTTAAGTTATTTATGCAAAAGTT
consensus      tggtttttaaagagttaagttacatatatttttctcacttaagttatttatgcaaaagtt
US-10-788-    533
US-10-788-    639
US-10-788-    643
US-10-788-    675
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US-10-788- 2197 TTCTGTGAGAGAAAGACAATGTTATATGCTTTATGAATTAAACAGTCTGTTCTTCCAGA
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US-10-788- 2197 TTCTGTGAGAGAAAGACAATGTTATATGCTTTATGAATTAAACAGTCTGTTCTTCCAGA
|||||
consensus      tttctgtagagaatgacaatgttaataattgtttatgaattaacacgtctgttcttccaga

US-10-788- 533
US-10-788- 639
US-10-788- 643
US-10-788- 675

US-10-788- 2258 GTCCAGAGACATTGTTAATAAAGACAATGAATCATGACCGAAAG
|||||
US-10-788- 2258 GTCCAGAGACATTGTTAATAAAGACAATGAATCATGACCGAAAG
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consensus      gtccagagacattgtttaataaagacaatgaatcatgaccgaaag
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Alignment score = -28949.00

Scoring matrix:

	1	2	3	4	5	6
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2			-7673	-7754	-7555	-8348
3				521	412	-54
4					396	-106
5						-249
6						

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42 ; Search time 10379.5 Seconds
(without alignments)
10741.894 Million cell updates/sec

Title: US-10-788-606-1

Perfect score: 2301

Sequence: 1 agagctgtgctactggaag.....caatgaatcatgaccggaag 2301

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:*

1: gb_pat*

2: gb_btg*

3: gb_in*

4: gb_om*

5: gb_ov*

6: gb_pat*

7: gb_ph*

8: gb_pl*

9: gb_pr*

10: gb_roi*

11: gb_sts*

12: gb_sy*

13: gb_un*

14: gb_vl*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2301	100.0	2301	6	BD251906	BD251906 Compositi
2	2301	100.0	2301	6	AR258992	AR258992 Sequence
3	2301	100.0	2301	6	AR267465	AR267465 Sequence
4	2301	100.0	2301	6	AR371665	AR371665 Sequence
5	2301	100.0	2301	9	AF326739	AF326739 Homo sapi
6	2299.4	99.9	2301	6	BD251907	BD251907 Compositi
7	2299.4	99.9	2301	6	BD251909	BD251909 Compositi
8	2299.4	99.9	2301	6	AR258993	AR258993 Sequence
9	2299.4	99.9	2301	6	AR258995	AR258995 Sequence
10	2299.4	99.9	2301	6	AR267466	AR267466 Sequence
11	2299.4	99.9	2301	6	AR267468	AR267468 Sequence
12	2299.4	99.9	2301	6	AR371666	AR371666 Sequence
13	2299.4	99.9	2301	6	AR371668	AR371668 Sequence
14	2297.8	99.9	2301	6	BD251908	BD251908 Compositi
15	2297.8	99.9	2301	6	AR258994	AR258994 Sequence
16	2297.8	99.9	2301	6	AR371667	AR371667 Sequence
17	2297.8	99.9	2301	6	AR371667	AR371667 Sequence
18	2280.6	99.1	2329	6	AX056687	AX056687 Sequence
19	2280.6	99.1	2329	6	AX574536	AX574536 Sequence

AY358627 Homo sapi
AF331844 Homo sapi
AX342535 Sequence
AX342537 Sequence
BD251915 Compositi
AR259001 Sequence
AR267474 Sequence
AR371674 Sequence
AR326736 Homo sapi
AC003098 Homo sapi
AC055813 Homo sapi
AF397423 Homo sapi
AC073954 Homo sapi
AY358203 Homo sapi
AX323453 Sequence
AR259025 Sequence
AR267498 Sequence
AR371698 Sequence
BD251910 Compositi
AR258996 Sequence
AR267469 Sequence
AR371669 Sequence
AF326742 Cercopith
BD251912 Compositi
AR258998 Sequence
AR267471 Sequence

ALIGNMENTS

RESULT 1
BD251906
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITILE
JOURNAL
COMMENT

BD251906
Compositions and methods for increasing bone mineralization.
BD251906.1 GI:33061676
JP 2002531090-A/1.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2301)
Paepker,B.W., Nese,J.V. and Winkler,D.G.
Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
Compositions and methods for increasing bone mineralization
Patent: JP 2002531090-A 1 24-SEP-2002;
DARWIN DISCOVERY LTD
OS Homo sapiens (human)
PN JP 2002531090-A/1
PD 24-SEP-2002
PF 24-NOV-1999 JP 2000585404
PI 27-NOV-1998 US 60/110283
PI MARY E BRUNKOW, DAVID J GALAS, BRIAN KOVACEVICH, JOHN T MULLIGAN,
PI BRYAN W PAEPPER, JEFFREY VAN NESS, DAVID G WINKLER PC
C12N15/09, C12N15/09, A01K67/027, A61K31/713, A61K48/00, A61P19/00, PC
A61P19/02,
PC C07K14/47, C07K16/18, C07K19/00, C12N5/10, C12N9/00, C12P21/02, PC
C12P21/08,
PC C12Q1/02, C12Q1/68, G01N33/53, G01N33/53, G01N33/566, C12N15/00, PC
C12N15/00,
PC C12N5/00
CC Compositions and methods for increasing bone mineralization FH
Key Location/Qualifiers
FT source 1. .2301
Location/Qualifiers
1. .2301
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

FEATURES
source
ORIGIN

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:05:42 ; Search time 8462.86 Seconds
(without alignments)

10349.440 Million cell updates/sec

Title: US-10-788-606-1

Perfect score: 2301

Sequence: 1 egagcgtgctactggaag.....caatgaatcatgaccgaaag 2301

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsal:*
9: gb_gsal2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1448.2	62.9	1475	3	AF170491 Homo sapi
2	1169.6	50.8	1177	3	AF184211 Homo sapi
3	668.4	29.0	685	5	BU617598 UI-H-DF0-
4	658.2	28.6	686	5	BU621845 UI-H-DF0-
5	642	27.9	642	9	AY400962 Homo sapi
6	550.4	23.9	637	9	AY400963 Pan trogl
7	527.2	22.9	1990	3	AK017295 Mus muscu
8	512.4	22.3	540	1	AF1768408 whl4C03.x
9	506.2	22.0	947	6	BY171106 BX171106
10	501.6	21.8	636	9	AY400964 Mus muscu
11	494	21.5	494	5	BX282099 BX282099
12	491.2	21.3	667	2	BB636457 BB636457
13	491	21.3	491	2	AW771508 hu57e09.x
14	469.4	20.4	623	2	BB637315 BB637315
15	457	19.9	468	1	AI498457 tm49e03.x
16	452	19.6	466	1	AI383985 te35f02.x
17	439.8	19.1	466	1	AI493134 qz50b02.x
18	428.4	18.6	452	1	AA393768 zv64f08.s
19	419.4	18.2	432	7	CN258789 170005325
20	387.4	16.8	414	1	AI498691 tm42C02.x
21	375.2	16.3	402	1	AA969408 op53b07.s
22	367	15.9	511	2	BB638050 BB638050
23	351.8	15.3	419	2	BE101082 UI-R-BJ1-
24	341	14.8	341	1	AI580267 tm45e09.x

C	25	335	14.6	352	2	BF431247	BF431247 naa42g09.
C	26	321.8	14.0	498	6	CB425970	CB425970 601084 MA
C	27	306.2	13.3	360	1	AI556282	AI556282 UI-R-C2p-
C	28	294	12.8	329	1	AI783624	AI783624 t299d03.x
C	29	278.2	12.1	704	6	CB418651	CB418651 591462 MA
C	30	264.2	11.5	269	7	CN258788	CN258788 170005328
C	31	260.6	11.3	535	8	AQ171546	AQ171546 HS_3088 B
C	32	256.6	11.2	732	9	CR823295	CR823295 GROAA53C
C	33	255.8	11.1	315	1	AI113131	AI113131 UI-R-C2p-
C	34	243	10.6	291	2	BE111224	BE111224 UI-R-BJ1-
C	35	233	10.1	548	7	CO620016	CO620016 D69-202a2
C	36	229.4	10.0	271	7	D79813	D79813 HUM330C08B
C	37	219.2	9.5	648	6	CB432800	CB432800 609052 MA
C	38	190.4	8.3	221	6	CD250782	CD250782 AGENCOURT
C	39	163.2	7.1	532	1	AL922835	AL922835 AL922835
C	40	161.2	7.0	180	1	AA393939	AA393939 zv64f09.x
C	41	158.8	6.9	254	2	BF523030	BF523030 UI-R-C2p-
C	42	153.8	6.7	643	2	BB221258	BB221258 BB221258
C	43	153.8	6.7	716	4	BJ712074	BJ712074 BJ712074
C	44	151.6	6.6	423	6	CB762755	CB762755 AMGNNUC:T
C	45	150	6.5	676	2	BB212560	BB212560 BB212560

ALIGNMENTS

RESULT 1	AF170491	1475 bp	mrna	linear	HTC 01-AUG-2003
LOCUS	AF170491	Homo sapiens	MSTP078	(MST078)	mrna, complete cds.
DEFINITION	AF170491	AF170491.1	GI:33337957		
ACCESSION	AF170491	HTC			
VERSION	AF170491.1	Homo sapiens (human)			
KEYWORDS	HTC				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 1475)			
AUTHORS	Hui R.T., Qin B.M., Sheng H., Liu Y.Q., Zhao B., Liu B., Wang X.Y., Zhang Q., Song L., Gao Y., Zhang C.L., Ye J., Ji X.J., Liu B.H., Lu H., Xu H.S., Chen J.Z., Cai M.Q., Zheng W.Y., Teng C.Y., Liu Q., Yu L.T., Lin J., Gong Q., Zhang A.M. and Gao R.L.				
TITLE	Homo sapiens normal aorta mRNA MST078				
JOURNAL	Unpublished				
REFERENCE	2	(bases 1 to 1475)			
AUTHORS	Hui R.T., Qin B.M., Sheng H., Liu Y.Q., Zhao B., Liu B., Wang X.Y., Zhang Q., Song L., Gao Y., Zhang C.L., Ye J., Ji X.J., Liu B.H., Lu H., Xu H.S., Chen J.Z., Cai M.Q., Zheng W.Y., Teng C.Y., Liu Q., Yu L.T., Lin J., Gong Q., Zhang A.M. and Gao R.L.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-JUL-1999)				
FEATURES	Cardiovascular Disease, Cardiovascular Institute, CAMS and PUMC, 167, Bei Li Shi Lu, Beijing 100037, P.R.China				
source	Location/Qualifiers				
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	275. .601				
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	/product="MSTP078"				
	/protein_id="AAQ13601.1"				
	/db_xref="GI:33337958"				
	/translation="MRAQSTRIGATVDVVSSPGSATNLCLNLEHNSPGPOFLCK				
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	SSDSQR"				
ORIGIN					
Query Match	62.9%	Score 1448.2	DB 3	Length 1475	

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42 ; Search time 1340.09 Seconds
(without alignments)
10164.517 Million cell updates/sec

Title: US-10-788-606-1
Perfect score: 2301
Sequence: 1 agagcctgtctactggaag.....caatgaatcatgacgcgaag 2301

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 16Dec04:*

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- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
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- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2301	100.0	2301	3	AAA29055 Human TGF
2	2301	100.0	2301	13	ADA12958 TGF-beta
3	2301	100.0	2323	10	ACF79824 Human SOS
4	2299.4	99.9	2301	3	AAA29061 Mutant hu
5	2299.4	99.9	2301	3	AAA29062 Human TGF
6	2299.4	99.9	2301	13	ADA12964 TGF-beta
7	2299.4	99.9	2301	13	ADA12960 TGF-beta
8	2297.8	99.9	2301	3	AAA29056 Human TGF
9	2297.8	99.9	2301	13	ADA12962 TGF-beta
10	2280.6	99.1	2329	4	AAA91023
11	2280.6	99.1	2329	6	ABK69992
12	2280.6	99.1	2329	9	ADA01331 Human PRO
13	2280.6	99.1	2329	9	ADA43760 Human CDN
14	2280.6	99.1	2329	9	ADA43528 Human CDN
15	2280.6	99.1	2329	9	ADA01203 Human PRO
16	2280.6	99.1	2329	9	ADA01087 Human CDN
17	2280.6	99.1	2329	9	ADA43644 Human CDN
18	2280.6	99.1	2329	9	ADA06906 Human PRO
19	2280.6	99.1	2329	9	ADA08394 Novel hum
20	2280.6	99.1	2329	9	ADB99687 Human PRO

21	2280.6	99.1	2329	9	ADB86970	ADB86970 Human PRO
22	2280.6	99.1	2329	9	ADB66125	ADB66125 Human CDN
23	2280.6	99.1	2329	10	ADB99803	ADB99803 Human PRO
24	2280.6	99.1	2329	10	ADB99458	ADB99458 Novel hum
25	2280.6	99.1	2329	10	ADB66009	ADB66009 Human CDN
26	2280.6	99.1	2329	10	ADC23407	ADC23407 Human CDN
27	2280.6	99.1	2329	10	ADC26100	ADC26100 Human PRO
28	2280.6	99.1	2329	10	ADE04927	ADE04927 Human PRO
29	2280.6	99.1	2329	10	ADE11233	ADE11233 Human PRO
30	2280.6	99.1	2329	10	ADD88164	ADD88164 Human PRO
31	2280.6	99.1	2329	10	ADD95459	ADD95459 Human CDN
32	2280.6	99.1	2329	10	ADE06389	ADE06389 Human PRO
33	2280.6	99.1	2329	10	ADE38164	ADE38164 Human PRO
34	2280.6	99.1	2329	10	ADD88280	ADD88280 Human PRO
35	2280.6	99.1	2329	10	ADD90861	ADD90861 Human CDN
36	2280.6	99.1	2329	10	ADF99416	ADF99416 Human CDN
37	2280.6	99.1	2329	10	ADG06509	ADG06509 Human PRO
38	2280.6	99.1	2329	10	ADG05460	ADG05460 Human PRO
39	2280.6	99.1	2329	10	ADG82461	ADG82461 Human PRO
40	2280.6	99.1	2329	12	ADE51714	ADE51714 Human CDN
41	2280.6	99.1	2329	12	ADE51830	ADE51830 Human CDN
42	2280.6	99.1	2329	12	ADE37688	ADE37688 Human CDN
43	2280.6	99.1	2329	12	ADE37572	ADE37572 Human CDN
44	2280.6	99.1	2329	12	ADD95343	ADD95343 Human CDN
45	2280.6	99.1	2329	12	ADE38043	ADE38043 Human PRO

ALIGNMENTS

RESULT 1
AAA29055
ID AAA29055 standard; cDNA; 2301 BP.
XX
AC AAA29055;
XX
DT 12-SEP-2000 (first entry)
XX
DE Human TGF-beta binding protein (BEER) cDNA.
XX
KW osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
KW BEER; chromosome 17q12-21; gene therapy; antisense therapy; fracture;
KW bone mineralization; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 48..689
FT /*tag= a
FT /product= "TGF-beta_binding_protein"
XX
PN WO200032773-A1.
XX
PD 08-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US027990.
XX
PR 27-NOV-1998; 98US-0110283P.
XX
PA (DARW-) DARWIN DISCOVERY LTD.
XX
PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;
PI Van Ness J, Winkler DG;
XX
XX WPI; 2000-412321/35.
XX P-PSDB; AAY96429.
XX
XX Nucleic acids (1) encoding a transforming growth factor beta binding
XX protein, useful for identifying agents for treating osteopenia,
XX osteoporosis and fractures.
XX
XX Claim 1; Page 114-115, 162pp; English.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:15:06 ; Search time 1539.09 Seconds
(without alignments)

9344.794 Million cell updates/sec

Title: US-10-788-606-1

Perfect score: 2301

Sequence: 1

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2301	100.0	2301	16	US-10-384-893-1 Sequence 1, Appli
2	2301	100.0	2301	17	US-10-463-190-1 Sequence 1, Appli
3	2301	100.0	2301	18	US-10-095-248A-1 Sequence 1, Appli
4	2301	100.0	2301	19	US-10-788-606-1 Sequence 1, Appli
5	2301	100.0	2301	21	US-10-799-162-1 Sequence 57, Appli
6	2301	100.0	2301	21	US-10-868-497-57 Sequence 2, Appli
7	2301	100.0	2323	17	US-10-377-315-2

8	2299.4	99.9	2301	16	US-10-384-893-3	Sequence 3, Appli
9	2299.4	99.9	2301	16	US-10-384-893-7	Sequence 7, Appli
10	2299.4	99.9	2301	17	US-10-463-190-3	Sequence 3, Appli
11	2299.4	99.9	2301	17	US-10-463-190-7	Sequence 7, Appli
12	2299.4	99.9	2301	18	US-10-095-248A-3	Sequence 3, Appli
13	2299.4	99.9	2301	18	US-10-095-248A-7	Sequence 7, Appli
14	2299.4	99.9	2301	18	US-10-788-606-3	Sequence 3, Appli
15	2299.4	99.9	2301	19	US-10-788-606-7	Sequence 7, Appli
16	2299.4	99.9	2301	21	US-10-799-162-3	Sequence 3, Appli
17	2299.4	99.9	2301	21	US-10-799-162-7	Sequence 7, Appli
18	2299.4	99.9	2301	21	US-10-868-497-61	Sequence 61, Appli
19	2297.8	99.9	2301	16	US-10-384-893-5	Sequence 5, Appli
20	2297.8	99.9	2301	17	US-10-463-190-5	Sequence 5, Appli
21	2297.8	99.9	2301	18	US-10-095-248A-5	Sequence 5, Appli
22	2297.8	99.9	2301	19	US-10-788-606-5	Sequence 5, Appli
23	2297.8	99.9	2301	21	US-10-799-162-5	Sequence 5, Appli
24	2297.8	99.9	2301	21	US-10-868-497-59	Sequence 59, Appli
25	2280.6	99.1	2329	14	US-10-245-752-63	Sequence 63, Appli
26	2280.6	99.1	2329	14	US-10-245-859-63	Sequence 63, Appli
27	2280.6	99.1	2329	14	US-10-245-103-63	Sequence 63, Appli
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29	2280.6	99.1	2329	14	US-10-245-143-63	Sequence 63, Appli
30	2280.6	99.1	2329	14	US-10-245-771-63	Sequence 63, Appli
31	2280.6	99.1	2329	14	US-10-245-851-63	Sequence 63, Appli
32	2280.6	99.1	2329	14	US-10-245-883-63	Sequence 63, Appli
33	2280.6	99.1	2329	14	US-10-237-535-63	Sequence 63, Appli
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36	2280.6	99.1	2329	14	US-10-238-370-63	Sequence 63, Appli
37	2280.6	99.1	2329	14	US-10-245-055-63	Sequence 63, Appli
38	2280.6	99.1	2329	14	US-10-245-147-63	Sequence 63, Appli
39	2280.6	99.1	2329	14	US-10-245-739-63	Sequence 63, Appli
40	2280.6	99.1	2329	14	US-10-245-739-63	Sequence 63, Appli
41	2280.6	99.1	2329	14	US-10-246-210-63	Sequence 63, Appli
42	2280.6	99.1	2329	14	US-10-239-196-63	Sequence 63, Appli
43	2280.6	99.1	2329	14	US-10-243-024-63	Sequence 63, Appli
44	2280.6	99.1	2329	14	US-10-243-409-63	Sequence 63, Appli
45	2280.6	99.1	2329	14	US-10-245-621-63	Sequence 63, Appli

ALIGNMENTS

RESULT 1

US-10-384-893-1
; Sequence 1, Application US/10384893
; Publication No. US20030166247A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepker, Bryan W.
; APPLICANT: Van Nessel, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
; FILE REFERENCE: 240083.508D5
; CURRENT APPLICATION NUMBER: US/10/384,893
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-384-893-1

Query Match 100.0%; Score 2301; DB 16; Length 2301;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGAGCCTGTGTACTTGGAGGTGGCGTSCCCTCTCTGTGTGGTACCATGAGTCCAC 60

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:55:24 ; Search time 9974.03 Seconds
(without alignments)
9417.841 Million cell updates/sec

Title: US-10-788-606-1

Perfect score: 2301

Sequence: 1 agagctgtctactggaag.....caatgaatcatgaccgaaag 2301

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA Main:*

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:03:06 ; Search time 404.818 Seconds
(without alignments)
9300.665 Million cell updates/sec

(without alignment)
9300.665 Million cell updates/sec

Title: US-10-788-606-1
 Perfect score: 2301
 Sequence: 1 aaagcctctgctactggaag.....caatgaatcatgaccgaaag 2301

perfect score: 2301
Sequence: 1 aaagcctgtcgtactggaag.....caatgaatcatgaccgaaag 2301

Sequence: 1 aaacccctgctactggaag.....caatgaatcatgaccgaaag 2301

Scoring table: IDENTITY_NUC

Gapop 10^{-1.0} , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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4: /cgn2_6/prodata/1/11a/6b_COMB.seq.*
5: /cgn2_6/prodata/1/11a/6bTTIS_COMB.seq.*
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3: /cgn2_6/ptodata/1/ima/fcgs.com:seq:
6: /cgn2_6/ptodata/1/ima/backfile1.seq:*
```

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2301	100.0	2301	3	US-09-449-2180-1	Sequence 1, A
2	2301	100.0	2301	4	US-09-668-529A-1	Sequence 1, A
3	2301	100.0	2301	4	US-09-668-037A-1	Sequence 1, A
4	2301	100.0	2301	4	US-09-668-021-1	Sequence 1, A
5	2299.4	99.9	2301	3	US-09-449-2180-3	Sequence 3, A
6	2299.4	99.9	2301	3	US-09-449-2180-7	Sequence 7, A
7	2299.4	99.9	2301	4	US-09-668-529A-3	Sequence 3, A
8	2299.4	99.9	2301	4	US-09-668-529A-7	Sequence 7, A
9	2299.4	99.9	2301	4	US-09-668-037A-3	Sequence 3, A
10	2299.4	99.9	2301	4	US-09-668-037A-7	Sequence 7, A
11	2299.4	99.9	2301	4	US-09-668-021-3	Sequence 3, A
12	2299.4	99.9	2301	4	US-09-668-021-7	Sequence 7, A
13	2297.8	99.9	2301	3	US-09-449-2180-5	Sequence 5, A
14	2297.8	99.9	2301	4	US-09-668-529A-5	Sequence 5, A
15	2297.8	99.9	2301	4	US-09-668-037A-5	Sequence 5, A
16	2297.8	99.9	2301	4	US-09-668-021-5	Sequence 5, A
17	2047.8	89.0	9301	3	US-09-449-2180-18	Sequence 18,
18	2047.8	89.0	9301	4	US-09-668-529A-18	Sequence 18,
19	2047.8	89.0	9301	4	US-09-668-037A-18	Sequence 18,
20	2047.8	89.0	9301	4	US-09-668-021-18	Sequence 18,
21	642	27.9	642	3	US-09-449-2180-45	Sequence 45,
22	642	27.9	642	4	US-09-668-529A-45	Sequence 45,
23	642	27.9	642	4	US-09-668-037A-45	Sequence 45,
24	613.2	26.6	642	3	US-09-449-2180-9	Sequence 9, A
25	613.2	26.6	642	4	US-09-668-529A-9	Sequence 9, A
26	613.2	26.6	642	4	US-09-668-037A-9	Sequence 9, A
27	613.2	26.6	642	4	US-09-668-021-9	Sequence 9, A

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42 ; Search time 10379.5 Seconds
(without alignments)
10741.894 Million cell updates/sec

Title: US-10-788-606-5

Perfect score: 2301

Sequence: 1 agagcctgtgctactggaag.....caatgaatcatgaccgaaaag 2301

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgtg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sta.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2301	100.0	2301	6	BD251908 Compositi
2	2301	100.0	2301	6	AR258994 Sequence
3	2301	100.0	2301	6	AR267467 Sequence
4	2301	100.0	2301	6	AR371667 Sequence
5	2299.4	99.9	2301	6	BD251909 Compositi
6	2299.4	99.9	2301	6	AR258995 Sequence
7	2299.4	99.9	2301	6	AR267468 Sequence
8	2299.4	99.9	2301	6	AR371668 Sequence
9	2297.8	99.9	2301	6	BD251906 Compositi
10	2297.8	99.9	2301	6	AR258992 Sequence
11	2297.8	99.9	2301	6	AR267465 Sequence
12	2297.8	99.9	2301	6	AR371665 Sequence
13	2297.8	99.9	2301	9	AF326739 Homo sapi
14	2296.2	99.8	2301	6	BD251907 Compositi
15	2296.2	99.8	2301	6	AR258993 Sequence
16	2296.2	99.8	2301	6	AR267466 Sequence
17	2296.2	99.8	2301	6	AR371666 Sequence
18	2277.4	99.0	2329	6	AX056687 Sequence
19	2277.4	99.0	2329	6	AX574536 Sequence

20	2277.4	99.0	2329	9	AY358627	Homo sapi
21	2270	98.7	2296	9	AF331844	Homo sapi
22	2245	97.6	2271	6	AX342535	Sequence
c	2047.8	89.0	7099	6	AX342537	Sequence
24	2047.8	89.0	9301	6	BD251915	Compositi
25	2047.8	89.0	9301	6	AR259001	Sequence
26	2047.8	89.0	9301	6	AR267474	Sequence
27	2047.8	89.0	9301	6	AR371674	Sequence
28	2047.8	89.0	21501	9	AF326736	Homo sapi
c	2047.8	89.0	94752	9	AC003098	Homo sapi
30	2035.8	88.5	80117	9	AC055813	Homo sapi
31	1612	70.1	93750	9	AF397423	Homo sapi
c	1066.4	46.3	177744	2	AC073954	Homo sapi
33	836.4	36.3	1154	9	AY358203	Homo sapi
34	755.8	32.8	759	6	AX323453	Sequence
35	638.8	27.8	642	6	AR259025	Sequence
36	638.8	27.8	642	6	AR267498	Sequence
37	638.8	27.8	642	6	AR371698	Sequence
38	610	26.5	642	6	BD251910	Compositi
39	610	26.5	642	6	AR258996	Sequence
40	610	26.5	642	6	AR267469	Sequence
41	610	26.5	642	6	AR371669	Sequence
42	610	26.5	642	9	AF326742	Cercopith
43	533	23.2	674	6	BD251912	Compositi
44	533	23.2	674	6	AR258998	Sequence
45	533	23.2	674	6	AR267471	Sequence

ALIGNMENTS

RESULT 1	BD251908	2301 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD251908	Compositions and methods for increasing bone mineralization.			
DEFINITION	BD251908	Compositions and methods for increasing bone mineralization.			
ACCESSION	BD251908	Compositions and methods for increasing bone mineralization.			
VERSION	BD251908.1	GI:33061678			
KEYWORDS	JP 2002531090-A/3.	Homo sapiens (human)			
SOURCE	Homo sapiens	Homo sapiens			
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 2301)	Brunkow, M.E., Galas, D.J., Kovacevich, B., Mulligan, J.T., Paepker, B.W., Ness, J.V. and Winkler, D.G.			
AUTHORS	1 (bases 1 to 2301)	Paepker, B.W., Ness, J.V. and Winkler, D.G.			
TITLE	Compositions and methods for increasing bone mineralization	Compositions and methods for increasing bone mineralization			
JOURNAL	Patent: JP 2002531090-A 3 24-SEP-2002;	DARWIN DISCOVERY LTD			
COMMENT	OS Homo sapiens (human)	PN JP 2002531090-A/3			
	PD 24-SEP-2002	PP 24-SEP-2002			
	PR 27-NOV-1998 US 60/110283	PI MARY E BRUNKOW, DAVID J GALAS, BRIAN KOVACEVICH, JOHN T MULLIGAN,			
	PI BRYAN W PAEPKER, JEFFREY VAN NESS, DAVID G WINKLER PC	C12N15/09, C12N15/09, A01K67/027, A61K31/713, A61K48/00, A61P19/00, PC			
	A61P19/02,	PC C07K14/47, C07K16/18, C07K19/00, C12N5/10, C12N9/00, C12P21/02, PC			
	C12P21/08,	PC C12Q1/02, C12Q1/68, G01N33/53, G01N33/53, G01N33/566, C12N15/00, PC			
	C12N15/00,	PC C12N5/00			
	CC Compositions and methods for increasing bone mineralization FH	FT key source 1. .2301			
	FT Location/Qualifiers	/organism="Homo sapiens"			
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ORIGIN					

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:05:42 ; Search time 8462.86 Seconds

(without alignments)
10349.440 Million cell updates/sec

Title: US-10-788-606-5

Perfect score: 2301

Sequence: 1 agagcgtgctactggaag.....caatgaatcatgacgagaag 2301

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1448.2	62.9	1475	3	AF170491 Homo sapi
2	1169.6	50.8	1177	3	AF184211 Homo sapi
3	658.4	29.0	685	5	BU617598 UI-H-DF0-
4	658.2	28.6	686	5	BU621845 UI-H-DF0-
5	538.8	27.8	642	9	AY400962 Homo sapi
6	547.2	22.8	637	9	AY400963 Pan trogl
7	527.2	22.9	1990	3	AK017295 Mus muscu
8	512.4	22.3	540	1	AI768408 wh14C03.x
9	506.2	22.0	947	6	BY17106 BX717106
10	501.6	21.8	636	9	AY400964 Mus muscu
11	491.2	21.3	667	2	BB636457
12	491.1	21.3	431	2	AW771508 hm57e09.x
13	490.8	21.3	494	5	EX282099 BX282099
14	469.4	20.4	623	2	BB637315
15	457	19.9	468	1	AI498457 tm49e03.x
16	452	19.6	466	1	AI498457 tm49e03.x
17	439.8	19.1	466	1	AI493134 q250b02.x
18	428.4	18.6	452	1	AA393768 z64f08.8
19	419.4	18.2	432	7	CN258789 170005325
20	387.4	16.8	414	1	AI498691 tm42c02.x
21	375.2	16.3	402	1	AA969408 op53b07.8
22	367	15.9	511	2	BB638050
23	351.8	15.3	419	2	BE101082
24	341	14.8	341	1	AI580267 tm45e09.x

C 25	335	14.6	352	2	BF431247	naa42909.
C 26	321.8	14.0	498	6	CB425970	601084 MA
C 27	306.2	13.3	360	1	AI556282	UI-R-C2P-
C 28	294	12.8	329	1	AI783624	t-99d03.x
29	278.2	12.1	704	6	CB418651	531462 MA
30	264.2	11.5	269	7	CN258788	170005328
C 31	257.4	11.2	535	8	AI71546	HS 3088_B
C 32	256.6	11.2	732	9	CR823295	GR0AA53C
C 33	255.8	11.1	315	1	AI113131	UI-R-C2P-
C 34	243	10.6	291	2	BE111224	UI-R-BJ1-
C 35	233	10.1	548	7	CO620016	DG9-202a2
36	229.4	10.0	271	7	D79813	HUM330C08B
37	219.2	9.5	648	6	CB432800	609052 MA
38	190.4	8.3	221	6	CD250782	AGENCOURT
39	161.6	7.0	532	1	AI922835	AL922835
40	161.2	7.0	180	1	AA393939	zv64f09.x
41	155.6	6.8	254	2	BF523030	UI-R-C2P-
42	153.8	6.7	643	2	BB221258	BB221258
43	153.8	6.7	716	4	BJ712074	BJ712074
44	150	6.5	676	2	BB212560	BB212560
45	148.4	6.4	423	6	CB762755	AMGNNUC:T

ALIGNMENTS

RESULT 1	AF170491	Homo sapiens	MSTP078	1475 bp	mRNA	linear	HTC 01-AUG-2003
LOCUS	AF170491	Homo sapiens	MSTP078	(MST078)	mRNA, complete cds.		
DEFINITION	AF170491	Homo sapiens	MSTP078	(MST078)	mRNA, complete cds.		
ACCESSION	AF170491.1	GI:33337957					
VERSION	AF170491.1	GI:33337957					
KEYWORDS	HTC.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	1 (bases 1 to 1475)						
AUTHORS	Hui,R.T., Qin,B.M., Sheng,H., Liu,Y.Q., Zhao,B., Liu,B., Wang,X.Y., Zhang,Q., Song,L., Gao,Y., Zhang,C.L., Ye,J., Ji,X.J., Liu,B.H., Lu,H., Xu,H.S., Chen,J.Z., Cai,M.Q., Zheng,W.Y., Teng,C.Y., Liu,Q., Yu,L.T., Lin,J., Gong,Q., Zhang,A.M. and Gao,R.L.						
TITLE	Homo sapiens normal aorta mRNA MST078						
JOURNAL	Unpublished						
REFERENCE	2 (bases 1 to 1475)						
AUTHORS	Hui,R.T., Qin,B.M., Sheng,H., Liu,Y.Q., Zhao,B., Liu,B., Wang,X.Y., Zhang,Q., Song,L., Gao,Y., Zhang,C.L., Ye,J., Ji,X.J., Liu,B.H., Lu,H., Xu,H.S., Chen,J.Z., Cai,M.Q., Zheng,W.Y., Teng,C.Y., Liu,Q., Yu,L.T., Lin,J., Gong,Q., Zhang,A.M. and Gao,R.L.						
TITLE	Direct Submission						
JOURNAL	Submitted (19-JUL-1999) Molecular Medicine Center for Cardiovascular Disease, Cardiovascular Institute, CAMS and PUMC, 167, Bei Li Shi Lu, Beijing 100037, P.R.China						
FEATURES	Location/Qualifiers						
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CDS	275..601	/db_xref="taxon:9606"					
	1..1475	/tissue type="aorta"					
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ORIGIN

Query Match

62.9%; Score 1448.2; DB 3; Length 1475;

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42 ; Search time 1340.09 Seconds
(without alignments)
10164.517 Million cell updates/sec

Title: US-10-788-606-5
Perfect score: 2301
Sequence: 1 agagctgtgctactggaag.....caatgaatcatgaccgaaag 2301

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870567 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2301	100.0	2301	3	AAA29056 Human TGF
2	2301	100.0	2301	13	ADSL12962 TGF-beta
3	2299.4	99.9	2301	3	AAA29062 Human TGF
4	2299.4	99.9	2301	13	ADSL12964 TGF-beta
5	2297.8	99.9	2301	3	AAA29055 Human TGF
6	2297.8	99.9	2301	13	ADSL12958 TGF-beta
7	2297.8	99.9	2323	10	ACF79824 Human SOS
8	2296.2	99.8	2301	3	AAA29061 TGF-beta
9	2296.2	99.8	2301	13	ADSL12960 TGF-beta
10	2277.4	99.0	2329	4	AAA91023 Human sec
11	2277.4	99.0	2329	6	ABK69992 CDNA enco
12	2277.4	99.0	2329	9	ADA01331 Human PRO
13	2277.4	99.0	2329	9	ADA43760 Human CDN
14	2277.4	99.0	2329	9	ADA43528 Human CDN
15	2277.4	99.0	2329	9	ADA01203 Human PRO
16	2277.4	99.0	2329	9	ADA01087 Human CDN
17	2277.4	99.0	2329	9	ADA43644 Human CDN
18	2277.4	99.0	2329	9	ADA06906 Human PRO
19	2277.4	99.0	2329	9	ADA08394 Novel hum
20	2277.4	99.0	2329	9	ADB99687 Human PRO

21	2277.4	99.0	2329	9	ADB86970 Human PRO
22	2277.4	99.0	2329	9	ADB66125 Human CDN
23	2277.4	99.0	2329	10	ADB99803 Human PRO
24	2277.4	99.0	2329	10	ADB99458 Novel hum
25	2277.4	99.0	2329	10	ADB66009 Human CDN
26	2277.4	99.0	2329	10	ADC23407 Human CDN
27	2277.4	99.0	2329	10	ADC26100 Human PRO
28	2277.4	99.0	2329	10	ADC04927 Human PRO
29	2277.4	99.0	2329	10	ADSL1233 Human PRO
30	2277.4	99.0	2329	10	ADD88164 Human PRO
31	2277.4	99.0	2329	10	ADD95459 Human CDN
32	2277.4	99.0	2329	10	ADRB06389 Human PRO
33	2277.4	99.0	2329	10	ADRB38164 Human PRO
34	2277.4	99.0	2329	10	ADRB8280 Human PRO
35	2277.4	99.0	2329	10	ADRB0861 Human CDN
36	2277.4	99.0	2329	10	ADF99416 Human CDN
37	2277.4	99.0	2329	10	ADG06509 Human PRO
38	2277.4	99.0	2329	10	ADG05460 Human PRO
39	2277.4	99.0	2329	10	ADG82461 Human PRO
40	2277.4	99.0	2329	12	ADSL1714 Human CDN
41	2277.4	99.0	2329	12	ADSL1830 Human CDN
42	2277.4	99.0	2329	12	ADSL37688 Human CDN
43	2277.4	99.0	2329	12	ADSL37572 Human CDN
44	2277.4	99.0	2329	12	ADD95343 Human CDN
45	2277.4	99.0	2329	12	ADSL38043 Human PRO

ALIGNMENTS

RESULT 1

AAA29056

ID AAA29056 standard; cDNA; 2301 BP.

XX AC AAA29056;

XX AC

DT 12-SEP-2000 (first entry)

DE Human TGF-beta binding protein (BEER) variant V101 cDNA.

KW osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
BEER; variant; V101; gene therapy; antisense therapy; fracture;
chromosome 17q12-21; bone mineralization; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 48..689

FT /*tag=

FT /label= BEER_variant V101

FT /product= "TGF-beta_binding_protein"

XX WO200032773-A1.

XX 08-JUN-2000.

XX 24-NOV-1999; 99WO-US027990.

XX 27-NOV-1998; 98US-0110283P.

XX (DARW-) DARWIN DISCOVERY LTD.

XX Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;

XX Van Ness J, Winkler DG;

XX WPI; 2000-412321/35.

XX P-PSDB; AAY96430.

XX Nucleic acids (1) encoding a transforming growth factor beta binding

XX protein, useful for identifying agents for treating osteopenia,

XX osteoporosis and fractures.

XX Claim 1; Page 118-119; 162pp; English.

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:15:06 ; Search time 1539.09 Seconds
(without alignments)

9344.794 Million cell updates/sec

Title: US-10-788-606-5

Perfect score: 2301

Sequence: 1 agagcctgtctactggaag.....caatgaatcatgaccgaaag 2301

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 26: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2301	100.0	2301	17	US-10-384-893-5
2	2301	100.0	2301	16	US-10-463-190-5
3	2301	100.0	2301	18	US-10-095-248A-5
4	2301	100.0	2301	19	US-10-788-606-5
5	2301	100.0	2301	21	US-10-799-162-5
6	2301	100.0	2301	21	US-10-868-497-59
7	2299.4	99.9	2301	16	US-10-384-893-7

8	2299.4	99.9	2301	17	US-10-463-190-7	Sequence 7, Appli
9	2299.4	99.9	2301	18	US-10-095-248A-7	Sequence 7, Appli
10	2299.4	99.9	2301	19	US-10-788-606-7	Sequence 7, Appli
11	2299.4	99.9	2301	21	US-10-799-162-7	Sequence 7, Appli
12	2299.4	99.9	2301	21	US-10-868-497-61	Sequence 61, Appl
13	2297.8	99.9	2301	16	US-10-384-893-1	Sequence 1, Appli
14	2297.8	99.9	2301	17	US-10-463-190-1	Sequence 1, Appli
15	2297.8	99.9	2301	18	US-10-095-248A-1	Sequence 1, Appli
16	2297.8	99.9	2301	19	US-10-788-606-1	Sequence 1, Appli
17	2297.8	99.9	2301	21	US-10-799-162-1	Sequence 1, Appli
18	2297.8	99.9	2301	21	US-10-868-497-57	Sequence 57, Appl
19	2297.8	99.9	2323	17	US-10-377-315-2	Sequence 2, Appli
20	2296.2	99.8	2301	16	US-10-384-893-3	Sequence 3, Appli
21	2296.2	99.8	2301	17	US-10-463-190-3	Sequence 3, Appli
22	2296.2	99.8	2301	18	US-10-095-248A-3	Sequence 3, Appli
23	2296.2	99.8	2301	19	US-10-788-606-3	Sequence 3, Appli
24	2296.2	99.8	2301	21	US-10-799-162-3	Sequence 3, Appli
25	2277.4	99.0	2329	14	US-10-245-752-63	Sequence 63, Appl
26	2277.4	99.0	2329	14	US-10-245-859-63	Sequence 63, Appl
27	2277.4	99.0	2329	14	US-10-245-103-63	Sequence 63, Appl
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29	2277.4	99.0	2329	14	US-10-245-143-63	Sequence 63, Appl
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39	2277.4	99.0	2329	14	US-10-245-730-63	Sequence 63, Appl
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ALIGNMENTS

RESULT 1

US-10-384-893-5
; Sequence 5, Application US/10384893
; Publication No. US20030166247A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galae, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepker, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
; FILE REFERENCE: BONE MINERALIZATION
; TITLE OF INVENTION: BONE MINERALIZATION
; FILE REFERENCE: 240083.508D5
; CURRENT APPLICATION NUMBER: US/10/384,893
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-384-893-5

Query Match 100.0%; Score 2301; DB 16; Length 2301;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:55:24 ; Search time 9974.03 Seconds
(without alignments)

9417.841 Million cell updates/sec

Title: US-10-788-606-5

Perfect score: 2301

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Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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OM nucleic - nucleic search, using sw model

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6348.430 Million cell updates/sec

Title: US-10-788-606-5
Perfect score: 2301
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Searched: 13027057 seqs, 223325459 residues

Total number of hits satisfying chosen parameters: 26054114

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2285.8	99.3	2302	15	US-60-680-473-44583
3	568.4	24.7	570	15	US-60-677-583-99
4	73.6	3.2	1089	15	US-60-680-544-23752
5	73.6	3.2	1089	15	US-60-680-473-23752
6	69.6	3.0	2337	1	PCT-US05-13260-1
7	60.6	2.6	39723	11	US-10-990-328A-96899
8	55.8	2.4	1216	15	US-60-669-241-24312
9	53.2	2.3	604	9	US-10-703-032-100242
10	53	2.3	1149	7	US-10-990-000-13
C 11	52.4	2.3	1917	9	US-10-703-032-28735
C 12	52.2	2.3	553	9	US-10-703-032-16224
C 13	52.2	2.3	1878	8	US-10-450-763-25120
C 14	52.2	2.3	3204	8	US-10-450-763-15861
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C 16	52.2	2.3	10178	13	US-11-031-175-977
C 17	51.6	2.2	586	9	US-10-703-032-53824
C 18	51.4	2.2	4830849	2	PCT-IB03-06509-1355

ALIGNMENTS

RESULT 1

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; Sequence 44583, Application US/60680544
; GENERAL INFORMATION:
; APPLICANT: Cooper, Matthew
; APPLICANT: Kinch, Deborah
; APPLICANT: Rosenberg, Michael
; APPLICANT: Subramaniam, S. Sai
; APPLICANT: Szak, Suzanne
; APPLICANT: Li, Huo
; APPLICANT: Bandaru, Raj
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
; TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
; FILE REFERENCE: 21590230000
; CURRENT APPLICATION NUMBER: US/60/680,544
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 48714
; SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 44583
; LENGTH: 2302
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-60-680-544-44583

Query Match 99.3%; Score 2285.8; DB 15; Length 2302;

Best Local Similarity 99.9%; Pred.No. 0;

Matches 2298; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:03:06 ; Search time 404.818 Seconds
(without alignments)
9300.665 Million cell updates/sec

Title: US-10-788-606-5

Perfect score: 2301

Sequence: 1 agagcctgtgctactggaag.....caatgaatcatgaccggaag 2301

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2301	100.0	2301	3	US-09-449-218D-5
2	2301	100.0	2301	4	US-09-668-529A-5
3	2301	100.0	2301	4	US-09-668-037A-5
4	2301	100.0	2301	4	US-09-668-021-5
5	2299.4	99.9	2301	3	US-09-449-218D-7
6	2299.4	99.9	2301	4	US-09-668-529A-7
7	2299.4	99.9	2301	4	US-09-668-037A-7
8	2299.4	99.9	2301	4	US-09-668-021-7
9	2297.8	99.9	2301	3	US-09-449-218D-1
10	2297.8	99.9	2301	4	US-09-668-529A-1
11	2297.8	99.9	2301	4	US-09-668-037A-1
12	2297.8	99.9	2301	4	US-09-668-021-1
13	2296.2	99.8	2301	3	US-09-449-218D-3
14	2296.2	99.8	2301	4	US-09-668-529A-3
15	2296.2	99.8	2301	4	US-09-668-037A-3
16	2296.2	99.8	2301	4	US-09-668-021-3
17	2047.8	89.0	9301	3	US-09-449-218D-18
18	2047.8	89.0	9301	4	US-09-668-529A-18
19	2047.8	89.0	9301	4	US-09-668-037A-18
20	2047.8	89.0	9301	4	US-09-668-021-18
21	638.8	27.8	642	3	US-09-449-218D-45
22	638.8	27.8	642	4	US-09-668-529A-45
23	638.8	27.8	642	4	US-09-668-037A-45
24	610	26.5	642	3	US-09-449-218D-9
25	610	26.5	642	4	US-09-668-529A-9
26	610	26.5	642	4	US-09-668-037A-9
27	610	26.5	642	4	US-09-668-021-9

28	533	23.2	674	3	US-09-449-218D-13	Sequence 13, Appl
29	533	23.2	674	4	US-09-668-529A-13	Sequence 13, Appl
30	533	23.2	674	4	US-09-668-037A-13	Sequence 13, Appl
31	533	23.2	674	4	US-09-668-021-13	Sequence 13, Appl
32	502	21.8	638	3	US-09-449-218D-11	Sequence 11, Appl
33	502	21.8	638	4	US-09-668-529A-11	Sequence 11, Appl
34	502	21.8	638	4	US-09-668-037A-11	Sequence 11, Appl
35	502	21.8	638	4	US-09-668-021-11	Sequence 11, Appl
36	466.2	20.3	532	3	US-09-449-218D-15	Sequence 15, Appl
37	466.2	20.3	532	4	US-09-668-529A-15	Sequence 15, Appl
38	466.2	20.3	532	4	US-09-668-037A-15	Sequence 15, Appl
39	466.2	20.3	532	4	US-09-668-021-15	Sequence 15, Appl
40	372.2	16.2	35828	3	US-09-449-218D-17	Sequence 17, Appl
41	372.2	16.2	35828	4	US-09-668-529A-17	Sequence 17, Appl
42	372.2	16.2	35828	4	US-09-668-037A-17	Sequence 17, Appl
43	372.2	16.2	35828	4	US-09-668-021-17	Sequence 17, Appl
44	190.2	8.3	196	4	US-09-513-999C-9816	Sequence 9816, Ap
45	82.6	3.6	962	3	US-09-188-930-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-449-218D-5
; Sequence 5, Application US/09449218D
; Patent No. 6395511
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepfer, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
; TITLE OF INVENTION: BONE MINERALIZATION
; FILE REFERENCE: 240083 508
; CURRENT APPLICATION NUMBER: US/09/449,218D
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-449-218D-5

Query Match	100.0%	Score 2301;	DB 3;	Length 2301;
Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 2301;	Conservative 0;	Gaps 0;		
QY	1	AGAGCCTGTGCTACTTGAAGTGGCGTCCCTCTCTGCTGTGTACCATGCTCCAC	60	
DB	1	AGAGCCTGTGCTACTTGAAGTGGCGTCCCTCTCTGCTGTGTACCATGCTCCAC	60	
QY	61	TGGCCCTGTGCTCATCTCCCTGTGGTACACAGCCTTCCGTGTAGTGGAGGCGG	120	
DB	61	TGGCCCTGTGCTCATCTCCCTGTGGTACACAGCCTTCCGTGTAGTGGAGGCGG	120	
QY	121	GTTGGCAGCGGTTCAAGATGATGCCAGGAATCATCCGCGAGCTCCGAGGTACCCG	180	
DB	121	GTTGGCAGCGGTTCAAGATGATGCCAGGAATCATCCGCGAGCTCCGAGGTACCCG	180	
QY	181	AGCCTCCAGCGAGCTTGAAGAACCAACAGCATATGACCGCGAGAACCGAGGCGG	240	
DB	181	AGCCTCCAGCGAGCTTGAAGAACCAACAGCATATGACCGCGCGAGAACCGAGGCGG	240	
QY	241	CTCCCCACCAACCCCTTTTGAGACCAAGAGCGTGTCCGAGTACAGTCCCGAGCTGACT	300	
DB	241	CTCCCCACCAACCCCTTTTGAGACCAAGAGCGTGTCCGAGTACAGTCCCGAGCTGACT	300	
QY	301	TCACCCGCTACGTGACCGATGGCGGTGGCGGACCGCCGAGCGGTACCGAGCTGGTGT	360	

Result No.	Score	Query Match	Length	DB	ID	Description
1	613.2	95.5	642	9	AY400962	AY400962 Homo sapi
2	528	82.2	637	9	AY400963	AY400963 Pan trogl
3	504.8	78.6	636	9	AY400964	AY400964 Mus muscu
4	504.8	78.6	1990	3	AK017295	AK017295 Mus muscu
5	483.8	75.4	947	6	BY171106	BY171106 BY171106
6	480	74.8	667	2	BB636457	BB636457 BB636457
7	458.2	71.4	623	2	BB637315	BB637315 BB637315
8	450.2	70.1	494	5	EX282099	EX282099 EX282099
9	378.6	59.0	1177	3	AF184211	AF184211 Homo sapi
10	355.8	55.4	511	2	BB638050	BB638050 BB638050
11	351.8	54.8	419	2	BE101082	BE101082 UI-R-BJ1-
12	307.8	47.9	360	1	AI556282	AI556282 UI-R-C2p-
13	259	40.3	315	1	AI113131	AI113131 UI-R-C2p-
14	246.2	38.3	291	2	BE111224	BE111224 UI-R-BJ1-
15	208.8	32.5	535	8	AQ171546	AQ171546 HS 3088 B
16	158.4	24.7	532	1	AL922835	AL922835 AL922835
17	152.2	23.7	716	4	BJ712074	BJ712074 BJ712074
18	145.4	22.6	254	2	BF523030	BF523030 UI-R-C2p-
19	141	22.0	749	6	CA374043	CA374043 648343 NC
20	140.4	21.9	423	6	CB762755	CB762755 AMGNNUC.T
21	130.2	20.3	1880	3	CR681743	CR681743 Tetradom
22	124.6	19.4	609	9	CR261683	CR261683 Reverse s
23	85.6	13.3	669	2	BF607657	BF607657 MY1_00059
24	84.2	13.1	854	6	BY707967	BY707967 BY707967

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42; Search time 373.896 Seconds
(without alignments)

10164.517 Million cell updates/sec

Title: US-10-788-606-9

Perfect score: 642

Sequence: 1 atcgagctccactggccct.....agctggagaacgctactag 642

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N Geneseq 16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1980s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
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3	642	100.0	642	13	ADI2966
4	613.2	95.5	642	3	AAA94051
5	613.2	95.5	642	12	ADI27109
6	613.2	95.5	759	6	ABA94293
7	613.2	95.5	2271	6	AA27576
8	613.2	95.5	2301	3	AAA29055
9	613.2	95.5	2301	13	ADI2958
10	613.2	95.5	2323	10	ACF79824
11	613.2	95.5	2329	4	AAA91023
12	613.2	95.5	2329	6	ABK69992
13	613.2	95.5	2329	9	ADA01331
14	613.2	95.5	2329	9	ADA43760
15	613.2	95.5	2329	9	ADA43528
16	613.2	95.5	2329	9	ADA01203
17	613.2	95.5	2329	9	ADA01087
18	613.2	95.5	2329	9	ADA43644
19	613.2	95.5	2329	9	ADA06906
20	613.2	95.5	2329	9	ADA08394

21	613.2	95.5	2329	9	ADB99687	AdB99687 Human PRO
22	613.2	95.5	2329	9	ADB86970	AdB86970 Human PRO
23	613.2	95.5	2329	9	ADB66125	AdB66125 Human PRO
24	613.2	95.5	2329	10	ADB99803	AdB99803 Human PRO
25	613.2	95.5	2329	10	ADB99458	AdB99458 Novel hum
26	613.2	95.5	2329	10	ADB66009	AdB66009 Human PRO
27	613.2	95.5	2329	10	ADC23407	AdC23407 Human PRO
28	613.2	95.5	2329	10	ADC26100	AdC26100 Human PRO
29	613.2	95.5	2329	10	ADBO4927	AdBO4927 Human PRO
30	613.2	95.5	2329	10	ADDE11233	AdE11233 Human PRO
31	613.2	95.5	2329	10	ADD88164	AdD88164 Human PRO
32	613.2	95.5	2329	10	ADD95459	AdD95459 Human PRO
33	613.2	95.5	2329	10	ADDE06389	AdE06389 Human PRO
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35	613.2	95.5	2329	10	ADD88280	AdD88280 Human PRO
36	613.2	95.5	2329	10	ADD90861	AdD90861 Human PRO
37	613.2	95.5	2329	10	ADP99416	AdP99416 Human PRO
38	613.2	95.5	2329	10	ADG08509	AdG08509 Human PRO
39	613.2	95.5	2329	10	ADG05460	AdG05460 Human PRO
40	613.2	95.5	2329	10	ADG82461	AdG82461 Human PRO
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44	613.2	95.5	2329	12	ADE37572	AdE37572 Human PRO
45	613.2	95.5	2329	12	ADD95343	AdD95343 Human PRO

ALIGNMENTS

RESULT 1

AAA29057

ID AAA29057 standard; CDNA; 642 BP.

XX

AC AAA29057;

XX

DT 12-SEP-2000 (first entry)

XX

DE Vervet TGF-beta binding protein (BEER) CDNA.

XX

KW osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization; ss.

XX

OS Cercopithecus pygerythrus.

XX

FH Key Location/Qualifiers

FT CDS

FT 1..642

FT /*tag= a

FT /product= "TGF-beta_binding_protein"

XX WO200032773-A1.

PN

XX

PD 08-JUN-2000.

XX

PP 24-NOV-1999; 99WO-US027990.

XX

PR 27-NOV-1998; 98US-0110283P.

XX

PA (DARW-) DARWIN DISCOVERY LTD.

XX

PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;

PI Van Ness J, Winkler DG;

XX WPI; 2000-412321/35.

DR

DR P-PSDB; AAY96431.

XX

PT Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures.

XX

PS Claim 1; Page 122; 162pp; English.

XX

CC This CDNA encodes a vervet transforming growth factor-beta (TGF-beta)

No.	Score	Match	length	ID	Description
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2	642	100.0	642	17	US-10-463-130-9
3	642	100.0	642	17	US-10-464-368-101
4	642	100.0	642	18	US-10-095-248A-9
5	642	100.0	642	19	US-10-788-606-9
6	642	100.0	642	21	US-10-799-162-9
7	642	100.0	642	21	US-10-868-497-63
8	642	100.0	642	16	US-10-384-893-9
9	642	100.0	642	17	US-10-463-130-9
10	642	100.0	642	17	US-10-464-368-101
11	642	100.0	642	18	US-10-095-248A-9
12	642	100.0	642	19	US-10-788-606-9
13	642	100.0	642	21	US-10-799-162-9
14	642	100.0	642	21	US-10-868-497-63
15	642	100.0	642	16	US-10-384-893-9
16	642	100.0	642	17	US-10-463-130-9
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21	642	100.0	642	21	US-10-868-497-63
22	642	100.0	642	16	US-10-384-893-9
23	642	100.0	642	17	US-10-463-130-9
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27	642	100.0	642	21	US-10-799-162-9
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29	642	100.0	642	16	US-10-384-893-9
30	642	100.0	642	17	US-10-463-130-9
31	642	100.0	642	17	US-10-464-368-101
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35	642	100.0	642	21	US-10-868-497-63
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37	642	100.0	642	17	US-10-463-130-9
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44	642	100.0	642	17	US-10-463-130-9
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46	642	100.0	642	18	US-10-095-248A-9
47	642	100.0	642	19	US-10-788-606-9
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62	642	100.0	642	21	US-10-

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:55:24 ; Search time 2782.85 Seconds
(without alignments)
9417.841 Million cell updates/sec

Title: US-10-788-606-9

Perfect score: 642

Sequence: 1 atcgagctccactggccct.....agctggagaacgcctactag 642

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3	544.4	84.8	570	15	US-60-677-583-99	Appl	Sequence 99, Appl
4	75.2	11.7	1089	15	US-60-680-544-23752	A	Sequence 23752, A
5	75.2	11.7	1089	15	US-60-680-473-23752	A	Sequence 23752, A
6	71	11.1	2337	1	PCR-US05-13260-1	Appl	Sequence 1, Appl
7	54.2	8.4	152132	11	US-10-940-774A-13845	A	Sequence 13845, A
8	54.2	8.4	152145	11	US-10-940-774A-12371	A	Sequence 12371, A
9	52.4	8.2	1917	9	US-10-703-033-28735	A	Sequence 28735, A
10	49.6	7.7	1149	7	US-10-990-000-13	Appl	Sequence 13, Appl
11	49.6	7.7	28493	13	US-11-031-175-1241	Ap	Sequence 1241, Ap
12	49.4	7.7	2323	11	US-10-990-328A-2709	Ap	Sequence 2709, Ap
13	49.4	7.7	2382	11	US-10-990-328A-2704	Ap	Sequence 2704, Ap
14	49.4	7.7	2440	11	US-10-990-328A-2707	Ap	Sequence 2707, Ap
15	49.4	7.7	2842	11	US-10-990-328A-2705	Ap	Sequence 2705, Ap
16	49.4	7.7	2701	11	US-10-990-328A-2706	Ap	Sequence 2706, Ap
17	49.4	7.7	25703	11	US-10-990-328A-97405	Ap	Sequence 97405, A
18	49.4	7.7	52112	11	US-10-990-328A-94429	Ap	Sequence 94429, A

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:03:06 ; Search time 112.948 Seconds
(without alignments)
9300.665 Million cell updates/sec

Title: US-10-788-606-9

Perfect score: 642
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	642	100.0	642	4	US-09-668-529A-9
3	642	100.0	642	4	US-09-668-037A-9
4	642	100.0	642	4	US-09-668-021-9
5	613.2	95.5	642	3	US-09-449-218D-45
6	613.2	95.5	642	4	US-09-668-529A-45
7	613.2	95.5	642	4	US-09-668-037A-45
8	613.2	95.5	2301	3	US-09-449-218D-1
9	613.2	95.5	2301	4	US-09-668-529A-1
10	613.2	95.5	2301	4	US-09-668-037A-1
11	613.2	95.5	2301	4	US-09-668-021-1
12	611.6	95.3	2301	3	US-09-449-218D-3
13	611.6	95.3	2301	3	US-09-449-218D-7
14	611.6	95.3	2301	4	US-09-668-529A-3
15	611.6	95.3	2301	4	US-09-668-529A-7
16	611.6	95.3	2301	4	US-09-668-037A-3
17	611.6	95.3	2301	4	US-09-668-037A-7
18	611.6	95.3	2301	4	US-09-668-021-3
19	611.6	95.3	2301	4	US-09-668-021-7
20	610	95.0	2301	3	US-09-449-218D-5
21	610	95.0	2301	4	US-09-668-529A-5
22	610	95.0	2301	4	US-09-668-037A-5
23	610	95.0	2301	4	US-09-668-021-5
24	530	82.6	674	3	US-09-449-218D-13
25	530	82.6	674	4	US-09-668-529A-13
26	530	82.6	674	4	US-09-668-037A-13
27	530	82.6	674	4	US-09-668-021-13

ALIGNMENTS

RESULT 1

US-09-449-218D-9

; Sequence 9, Application US/09449218D

; Patent No. 6395511

; GENERAL INFORMATION:

; APPLICANT: Brunkow, Mary E.

; APPLICANT: Galas, David J.

; APPLICANT: Kovacevich, Brian

; APPLICANT: Mulligan, John T.

; APPLICANT: Paepfer, Bryan W.

; APPLICANT: Van Ness, Jeffrey

; APPLICANT: Winkler, David G.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING

; BONE MINERALIZATION

; FILE REFERENCE: 240083.508

; CURRENT APPLICATION NUMBER: US/09/449,218D

; CURRENT FILING DATE: 1999-11-24

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: Fast-Seq for Windows Version 3.0

; SEQ ID NO 9

; LENGTH: 642

; TYPE: DNA

; ORGANISM: Cercopithecus pygerythrus

; US-09-449-218D-9

Query Match 100.0%; Score 642; DB 3; Length 642;

Best Local Similarity 100.0%; Pred. No. 7.6e-136;

Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAGCTCCACCTGGCCCTGTGCTTGTCTGCTGTGTACAGCAGCCTTCGGTGA 60

QY 61 GTGAGGCGCCAGGGTGGAGCCCTTCAAGATGATGACCAAGAAATCATCCCGAGCTC 120

DB 61 GTGAGGCGCCAGGGTGGAGCCCTTCAAGATGATGACCAAGAAATCATCCCGAGCTC 120

QY 121 GGAGAGTACCCCGAGCCTCCACCGAGCTGGAGAACCAAGACCATCAACCGCGGAG 180

DB 121 GGAGAGTACCCCGAGCCTCCACCGAGCTGGAGAACCAAGACCATCAACCGCGGAG 180

QY 181 AATGAGGCGCGCCTCCCGACCCCTTTGAGACCAAGAGCGTTCGAGTACAGCTGC 240

DB 181 AATGAGGCGCGCCTCCCGACCCCTTTGAGACCAAGAGCGTTCGAGTACAGCTGC 240

QY 241 CGAGAGCTGCACTTCACCCGCTAGTGACCGATGGCCCGAGCGCCAGCAGCTC 300

DB 241 CGAGAGCTGCACTTCACCCGCTAGTGACCGATGGCCCGAGCGCCAGCAGCTC 300

QY 301 ACCGAGTTGTTGCTCCGGCCAGTGGCGGCCGCGCCTGCTGCCCAACGCCATCGGC 360

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QY 360

DB 360

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DB 360

QY 360

DB 360

QY 360

DB 360

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DB 360

QY 360

DB 360

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42 ; Search time 2877.93 Seconds
(without alignments)
10741.894 Million cell updates/sec

Title: US-10-788-606-11

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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	638	100.0	638	6	AR267470	AR267470 Sequence
4	638	100.0	638	6	AR371670	AR371670 Sequence
5	638	100.0	638	10	AF326740	AF326740 Mus muscu
6	634.4	99.4	636	6	AX323455	AX323455 Sequence
7	556	87.1	674	6	BD251912	BD251912 Compositi
8	556	87.1	674	6	AR258998	AR258998 Sequence
9	556	87.1	674	6	AR267471	AR267471 Sequence
10	556	87.1	674	6	AR371671	AR371671 Sequence
11	556	87.1	674	10	AF326741	AF326741 Rattus no
12	503.2	78.9	642	6	BD251910	BD251910 Compositi
13	503.2	78.9	642	6	AR258996	AR258996 Sequence
14	503.2	78.9	642	6	AR267469	AR267469 Sequence
15	503.2	78.9	642	6	AR371669	AR371669 Sequence
16	503.2	78.9	642	9	AF326742	AF326742 Cercopith
17	502	78.7	759	6	AX323453	AX323453 Sequence
18	502	78.7	2271	6	AX342535	AX342535 Sequence
19	502	78.7	2296	9	AF331844	AF331844 Homo sapi

20	502	78.7	2301	6	BD251906	BD251906 Compositi
21	502	78.7	2301	6	BD251908	BD251908 Compositi
22	502	78.7	2301	6	AR258992	AR258992 Sequence
23	502	78.7	2301	6	AR258994	AR258994 Sequence
24	502	78.7	2301	6	AR267465	AR267465 Sequence
25	502	78.7	2301	6	AR267467	AR267467 Sequence
26	502	78.7	2301	6	AR371665	AR371665 Sequence
27	502	78.7	2301	6	AR371667	AR371667 Sequence
28	502	78.7	2323	9	AF326739	AF326739 Homo sapi
29	502	78.7	2329	6	AX056687	AX056687 Sequence
30	502	78.7	2329	6	AX574536	AX574536 Sequence
31	502	78.7	2329	9	AY358627	AY358627 Homo sapi
32	500.4	78.4	2301	6	BD251907	BD251907 Compositi
33	500.4	78.4	2301	6	BD251909	BD251909 Compositi
34	500.4	78.4	2301	6	AR258993	AR258993 Sequence
35	500.4	78.4	2301	6	AR258995	AR258995 Sequence
36	500.4	78.4	2301	6	AR267466	AR267466 Sequence
37	500.4	78.4	2301	6	AR267468	AR267468 Sequence
38	500.4	78.4	2301	6	AR371666	AR371666 Sequence
39	500.4	78.4	2301	6	AR371668	AR371668 Sequence
40	500	78.4	642	6	AR259025	AR259025 Sequence
41	500	78.4	642	6	AR267498	AR267498 Sequence
42	500	78.4	642	6	AR371698	AR371698 Sequence
43	464	72.7	1154	9	AY358203	AY358203 Homo sapi
44	427	66.9	35828	6	BD251914	BD251914 Compositi
45	427	66.9	35828	6	AR259000	AR259000 Sequence

ALIGNMENTS

RESULT 1	BD251911	638 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD251911	Compositions and methods for increasing bone mineralization.			
DEFINITION	BD251911	Compositions and methods for increasing bone mineralization.			
ACCESSION	BD251911.1	GI:33061681			
VERSION	JP 2002531090-A/6.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 638)				
AUTHORS	Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T., Paepker,B.W., Ness,J.V. and Winkler,D.G.				
TITLE	Compositions and methods for increasing bone mineralization				
JOURNAL	Patent: JP 2002531090-A 6 24-SEP-2002;				
COMMENT	DARWIN DISCOVERY LTD OS Mus musculus (mouse) PN JP 2002531090-A/6 PD 24-SEP-2002 PF 24-NOV-1999 JP 2000585404 PR 27-NOV-1998 US 60/110283 PI MARY E BRUNKOW, DAVID J GALAS, BRIAN KOVACEVICH, JOHN T MULLIGAN, PI BRYAN W PAEPKER, JEFFREY VAN NESS, DAVID G WINKLER PC C12N15/09, C12N15/09, A01K67/027, A61K48/00, A61P19/00, PC A61P19/02, PC C07K14/47, C07K16/18, C07K19/00, C12N5/10, C12N9/00, C12P21/02, PC C12P21/08, C12Q1/02, C12Q1/68, G01N33/53, G01N33/566, C12N15/00, PC C12N15/00, PC C12N5/00 CC Compositions and methods for increasing bone mineralization FH Key Location/Qualifiers FT source 1. .638 FT Location/Qualifiers source 1. .638 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090"				
FEATURES					
ORIGIN					

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1	636.4	99.7	1990	3	AK017295	Mus muscu
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3	615.4	96.5	947	6	BY17106	BY17106
4	606.4	95.0	667	2	BB636457	BB636457
5	581.4	91.1	623	2	BB637315	BB637315
6	500	78.4	642	9	AY400962	Homo sapi
7	467.8	73.3	511	2	BB638050	BB638050
8	416.4	65.1	637	9	AY400963	Pan trogl
9	389.8	61.1	419	2	BE101082	UI-R-BJ1
10	346.6	54.3	494	5	CB282099	CB282099
11	340.6	53.4	1177	3	AF184211	Homo sapi
12	335	52.5	360	1	AI556282	UI-R-C2p
13	289.4	45.4	315	1	AI113131	UI-R-C2p
14	273.4	42.9	291	2	BE111224	UI-R-BJ1
15	152.4	23.9	716	4	BJ712074	BJ712074
16	150	23.5	609	9	CR261683	Reverse
17	145	22.7	749	6	CA374043	CA374043
18	138.8	21.8	535	8	AQ171546	HS 3088
19	137.2	21.5	532	1	AL922835	AL922835
20	136.2	21.3	254	2	BF523030	UI-R-C2p
21	124.8	19.6	1880	3	CB681743	Tetradon
22	123.2	19.3	423	6	CB762755	AMGNNUC
23	84.8	13.3	854	6	BY079567	BY079567
24	84.8	13.3	979	6	BY702931	BY702931

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42 ; Search time 371.567 Seconds
(without alignments)
10164.517 Million cell updates/sec

Title: US-10-788-606-11

Perfect score: 638
Sequence: 1 atcgagccctactagcccc.....ctggagacgctactagag 638

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	634.4	99.4	636	6	Abas4294 Mouse clo
5	634.4	99.4	636	10	Acf79826 Mouse SOS
6	607	95.1	675	12	Adi27108 Mouse LRP
7	556	87.1	674	3	Aaa29059 Rat TGF-b
8	556	87.1	674	10	Acf79827 Rat TGF-b
9	556	87.1	674	12	Adi27113 Rat TGF-b
10	556	87.1	674	13	Adi2970 TGF-beta
11	503.2	78.9	642	3	Aaa29057 Vervet TG
12	503.2	78.9	642	12	Adi27200 Monkey LR
13	503.2	78.9	642	13	Ada12966 TGF-beta
14	502	78.7	759	6	Abas4293 Human clo
15	502	78.7	2271	6	Aad27576 Human ost
16	502	78.7	2301	3	Aaa29056 Human TGF
17	502	78.7	2301	3	Aaa29055 Human TGF
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ALIGNMENTS

RESULT 1

AAA29058

ID AAA29058 standard; cDNA; 638 BP.

XX

AC AAA29058;

XX

DT 12-SEP-2000 (first entry)

XX

DE Murine TGF-beta binding protein (BBER) cDNA.

XX

XX osteopathic; transforming growth factor-beta; TGF-beta; binding protein;

KW BBER; gene therapy; antisense therapy; fracture; bone mineralization; ss.

XX

OS Mus musculus.

XX

XX Key Location/Qualifiers

FT CDS l..636

FT /*tag= 'a

FT /product= "TGF-beta_binding_protein"

XX

PN WO200032773-A1.

XX

PD 08-JUN-2000.

XX

PF 24-NOV-1999; 99WO-US027990.

XX

PR 27-NOV-1998; 98US-0110283P.

XX

PA (DARW-) DARWIN DISCOVERY LTD.

XX

PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;

XX

PI Van Ness J, Winkler DG;

XX

XX WPI; 2000-412321/35.

DR P-PSDB; AAY96432.

XX

XX Nucleic acids (I) encoding a transforming growth factor beta binding

PT protein, useful for identifying agents for treating osteopenia,

PT osteoporosis and fractures.

XX

PS Claim 1; Page 123; 162pp; English.

XX

CC This cDNA encodes a murine transforming growth factor-beta (TGF-beta)

QV 1 ATGAGCCCTCACTAGCCCCGTGCCCTCATCTGCCCTACTTGTGCACGTCGCTTCTGTGCT 60

Query Match 100.0%; Score 638; DB 16; Length 638;
Best Local Similarity 100.0%; Pred. No. 5.3e-164;

RESULT 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:55:24 ; Search time 2765.51 Seconds
(without alignments)
9417.841 Million cell updates/sec

Title: US-10-788-606-11

Perfect score: 638

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Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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4	69.8	10.9	1089	15	US-60-680-544-23752	Sequence 23752, A	
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6	67.2	10.5	2337	1	PCT-0503-13260-1	Sequence 1, Appl	
7	53.2	8.3	2184	15	US-60-680-544-46033	Sequence 46033, A	
8	53.2	8.3	2184	15	US-60-680-473-46033	Sequence 46033, A	
9	50	7.8	4830849	2	PCT-IB03-06509-1355	Sequence 1355, Ap	
10	49.8	7.8	927	13	US-11-031-175-9087	Sequence 9087, Ap	
11	49.8	7.8	11963	13	US-11-031-175-1072	Sequence 1072, Ap	
12	48.2	7.6	553	9	US-10-703-032-730	Sequence 730, App	
13	46.4	7.3	1146	13	US-11-031-175-5791	Sequence 5791, Ap	
14	46.4	7.3	1216	13	US-60-689-241-24312	Sequence 24312, A	
15	46.4	7.3	2575	12	US-11-097-143-20867	Sequence 20867, A	
16	46.4	7.3	4794	12	US-11-097-143-20866	Sequence 20866, A	
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:03:06 ; Search time 112.244 Seconds
(without alignments)
9300.665 Million cell updates/sec

Title: US-10-788-606-11

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 11, Application US/09449218D

; Patent No. 6395511

; GENERAL INFORMATION:

; APPLICANT: Brunkow, Mary E.

; APPLICANT: Galas, David J.

; APPLICANT: Kovacevich, Brian

; APPLICANT: Mulligan, John T.

; APPLICANT: Paepker, Bryan W.

; APPLICANT: Van Ness, Jeffrey

; APPLICANT: Winkler, David G.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING

; TITLE OF INVENTION: BONE MINERALIZATION

; FILE REFERENCE: 240083.508

; CURRENT APPLICATION NUMBER: US/09/449,218D

; CURRENT FILING DATE: 1999-11-24

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 11

; LENGTH: 638

; TYPE: DNA

; ORGANISM: Mus musculus

; US-09-449-218D-11

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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
Maximum Match 100%
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9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	674	100.0	674	6	BD251912
2	674	100.0	674	6	AR258998
3	674	100.0	674	6	AR267471
4	674	100.0	674	6	AR371671
5	674	100.0	674	10	AF326741
6	557.6	82.7	636	6	AX323455
7	556	82.5	638	6	BD251911
8	556	82.5	638	6	AR258997
9	556	82.5	638	6	AR267470
10	556	82.5	638	6	AR371670
11	556	82.5	638	10	AF326740
12	536.2	79.6	759	6	AX323453
13	536.2	79.6	2236	9	AF331844
14	536.2	79.6	2301	6	BD251906
15	536.2	79.6	2301	6	AR258992
16	536.2	79.6	2301	6	AR267465
17	536.2	79.6	2301	6	AR371665
18	536.2	79.6	2323	9	AF326739
19	536.2	79.6	2323	6	AX056687

20	536.2	79.6	2329	6	AX574536	Sequence
21	536.2	79.6	2329	9	AY358627	Homo sapi
22	534.6	79.3	2301	6	BD251907	Compositi
23	534.6	79.3	2301	6	BD251909	Compositi
24	534.6	79.3	2301	6	AR258993	Sequence
25	534.6	79.3	2301	6	AR258995	Sequence
26	534.6	79.3	2301	6	AR267466	Sequence
27	534.6	79.3	2301	6	AR267468	Sequence
28	534.6	79.3	2301	6	AR371666	Sequence
29	534.6	79.3	2301	6	AR371668	Sequence
30	533	79.1	2301	6	BD251908	Compositi
31	533	79.1	2301	6	AR258994	Sequence
32	533	79.1	2301	6	AR267467	Sequence
33	533	79.1	2301	6	AR371667	Sequence
34	531.6	78.9	2271	6	AX342535	Sequence
35	530	78.6	642	6	BD251910	Compositi
36	530	78.6	642	6	AR258996	Sequence
37	530	78.6	642	6	AR267469	Sequence
38	530	78.6	642	6	AR371669	Sequence
39	530	78.6	642	9	AF326742	Cercopith
40	525.2	77.9	642	6	AR259025	Sequence
41	525.2	77.9	642	6	AR267498	Sequence
42	525.2	77.9	642	6	AR371698	Sequence
43	499.8	74.2	1154	9	AY358203	Homo sapi
44	428.2	63.5	226328	2	AC098160	Rattus no
45	428.2	63.5	236068	2	AC121721	Rattus no

ALIGNMENTS

RESULT 1	BD251912	BD251912	674 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	Compositions and methods for increasing bone mineralization.					
DEFINITION	BD251912					
ACCESSION	BD251912.1	GI:33061682				
VERSION	JP 2002531090-A/7					
KEYWORDS	Rattus norvegicus (Norway rat)					
SOURCE	Rattus norvegicus					
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
REFERENCE	1 (bases 1 to 674)					
AUTHORS	Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T., Paepker,B.W., Ness,J.V. and Winkler,D.G.					
TITLE	Compositions and methods for increasing bone mineralization					
JOURNAL	Patent: JP 2002531090-A 7 24-SEP-2002; DARWIN DISCOVERY LTD					
COMMENT	OS Rattus norvegicus (rat) PN JP 2002531090-A/7 PD 24-SEP-2002 PF 24-NOV-1999 JP 2000585404 PR 27-NOV-1998 US 60/110283 PI MARY E BRUNKOW,DAVID J GALAS,BRIAN KOVACEVICH,JOHN T MULLIGAN, PI BRYAN W PAEPKER,JEFFREY VAN NESS,DAVID G WINKLER PC C12N15/09,C12N15/09,A01K67/027,A61K31/713,A61K48/00,A61P19/00, PC A61P19/02, PC C07K14/47,C07K16/18,C07K19/00,C12N5/10,C12N9/00,C12P21/02, PC C12P21/08, PC C12Q1/02,C12Q1/68,G01N33/53,G01N33/53,G01N33/566,C12N15/00, PC C12N15/00, PC C12N5/00 CC Compositions and methods for increasing bone mineralization PH Key Location/Qualifiers FT source 1..674 FT /organism='Rattus norvegicus (rat)'. Location/Qualifiers 1..674 /organism='Rattus norvegicus' /mol_type='genomic DNA' /db_xref='taxon:10116'					
FEATURES	source					
ORIGIN						

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:05:42 ; Search time 2478.91 Seconds
(without alignments)
10349.440 Million cell updates/sec

Title: US-10-788-606-13

Perfect score: 674
Sequence: 1 gaggaccagtcgccccttct.....agctggagaagcctactag 674

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	570.2	84.6	1990	3	AK017295	AK017295 Mus muscu
2	557.6	82.7	636	9	AY400964	AY400964 Mus muscu
3	549.2	81.5	947	6	BY717106	BY717106 BY717106
4	542.2	80.4	667	2	BB636457	BB636457 BB636457
5	525.2	77.9	642	9	AY400962	AY400962 Homo sapi
6	518.8	77.0	623	2	BB637315	BB637315 BB637315
7	443.2	65.8	637	9	AY400963	AY400963 Pan trogl
8	419	62.6	419	2	BE101082	BE101082 UI-R-BJ1-
9	408.4	60.6	511	2	BB638050	BB638050 BB638050
10	382.8	56.8	494	5	EX282099	EX282099 EX282099
11	355.8	52.8	360	1	AI556282	AI556282 UI-R-C2p-
12	343.4	50.9	1177	3	AF184211	AF184211 Homo sapi
13	305.4	45.3	315	1	AI113131	AI113131 UI-R-C2p-
14	286.2	42.5	291	2	BE111224	BE111224 UI-R-BJ1-
15	218.2	32.4	254	2	BF523030	BF523030 UI-R-C2p-
16	199.4	29.6	423	6	CB762755	CB762755 AMGNNUC-T
17	167	24.8	535	8	AQ171546	AQ171546 HS 3088 B
18	152.2	22.6	716	4	BJ712074	BJ712074 BJ712074
19	152	22.6	532	1	AL922835	AL922835 AL922835
20	148.4	22.0	749	6	CA374043	CA374043 648343 NC
21	142	21.1	609	9	CR261683	CR261683 Reverse s
22	123.4	18.3	1880	3	CF681743	CF681743 Tetradon
23	84.4	12.5	854	6	BY707967	BY707967 BY707967
24	84.4	12.5	979	6	BY702931	BY702931 BY702931

25	84.4	12.5	988	6	BY702775	BY702775 BY702775
26	84.4	12.5	995	6	BY707897	BY707897 BY707897
27	84.4	12.5	1612	3	AK002396	AK002396 Mus muscu
28	84.4	12.5	1613	3	AK007893	AK007893 Mus muscu
29	84.4	12.5	1690	3	AK002240	AK002240 Mus muscu
30	84.4	12.5	1691	3	AK007967	AK007967 Mus muscu
31	83.6	12.4	669	2	BF607657	BF607657 MY1 00059
32	82	12.2	472	2	BF420024	BF420024 UI-R-BJ2-
33	82	12.2	532	2	BF407514	BF407514 UI-R-BJ2-
34	82	12.2	575	7	CK625985	CK625985 mj16902.y
35	82	12.2	621	7	CK626761	CK626761 mj25H07.y
36	81	12.0	385	2	AW434705	AW434705 UI-R-BJ0p
37	81	12.0	584	7	CF169948	CF169948 B0820E07-
38	80.4	11.9	607	7	CF951492	CF951492 UI-M-HL0-
39	80.2	11.9	799	6	CD742451	CD742451 UI-M-A00-
40	78.8	11.7	623	4	BI143761	BI143761 602907224
41	78	11.6	789	3	AK007935	AK007935 Mus muscu
42	77	11.4	723	4	BJ731200	BJ731200 BJ731200
43	76.4	11.3	687	4	BI081999	BI081999 602879836
44	75	11.1	355	1	AA197904	AA197904 mv05C05.r
45	75	11.1	433	1	AA067619	AA067619 mm23s07.r

ALIGNMENTS

RESULT 1	AK017295	1990 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430411E23 product:scierostin, full insert sequence.				
DEFINITION	AK017295				
ACCESSION	AK017295.1	GI:12856464			
VERSION	HTC; CAP trapper.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
MEDLINE	11076861				
PUBMED	11076861				
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42 ; Search time 392.533 Seconds

(without alignments)
10164.517 Million cell updates/sec

Title: US-10-788-606-13

Perfect score: 674

Sequence: 1 gaggaccgagtgcccttctt.....agctggagaagcctactactg 674

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	674	100.0	674	3	AAA29059 Rat TGF-b
2	674	100.0	674	10	ACF79827 Rat SOST
3	674	100.0	674	12	ADI27113 Rat LRP b
4	674	100.0	674	13	ADI2970 TGF-beta
5	557.6	82.7	636	6	ABA94294 Mouse clo
6	557.6	82.7	636	10	ACF79826
7	556	82.5	636	12	ADI27106 Mouse LRP
8	556	82.5	638	3	AAA29058 Murine TG
9	556	82.5	638	13	ADI27106 TGF-beta
10	536.2	79.6	759	6	ABA94293
11	536.2	79.6	2301	3	AAA29055 Human TGF
12	536.2	79.6	2301	13	ADI2958 TGF-beta
13	536.2	79.6	2323	10	ACF79824
14	536.2	79.6	2329	4	AAA91023
15	536.2	79.6	2329	6	ABK69992
16	536.2	79.6	2329	9	ADA01331
17	536.2	79.6	2329	9	ADA43760
18	536.2	79.6	2329	9	ADA43528 Human CDN
19	536.2	79.6	2329	9	ADA01203
20	536.2	79.6	2329	9	ADA01087 Human CDN

21	536.2	79.6	2329	9	ADA43644	Ada43644 Human CDN
22	536.2	79.6	2329	9	ADA06906	Ada06906 Human PRO
23	536.2	79.6	2329	9	ADA08394	Ada08394 Novel hum
24	536.2	79.6	2329	9	ADB99687	ADB99687 Human PRO
25	536.2	79.6	2329	9	ADB86970	ADB86970 Human PRO
26	536.2	79.6	2329	9	ADB66125	ADB66125 Human CDN
27	536.2	79.6	2329	10	ADB99803	ADB99803 Human PRO
28	536.2	79.6	2329	10	ADB99458	ADB99458 Novel hum
29	536.2	79.6	2329	10	ADB66009	ADB66009 Human CDN
30	536.2	79.6	2329	10	ADC23407	ADC23407 Human CDN
31	536.2	79.6	2329	10	ADC26100	ADC26100 Human PRO
32	536.2	79.6	2329	10	ADE04927	ADE04927 Human PRO
33	536.2	79.6	2329	10	ADE11233	ADE11233 Human PRO
34	536.2	79.6	2329	10	ADD88164	ADD88164 Human PRO
35	536.2	79.6	2329	10	ADD95459	ADD95459 Human CDN
36	536.2	79.6	2329	10	ADE06389	ADE06389 Human PRO
37	536.2	79.6	2329	10	ADE38164	ADE38164 Human PRO
38	536.2	79.6	2329	10	ADD88280	ADD88280 Human PRO
39	536.2	79.6	2329	10	ADD90861	ADD90861 Human CDN
40	536.2	79.6	2329	10	ADF99416	ADF99416 Human CDN
41	536.2	79.6	2329	10	ADG06509	ADG06509 Human PRO
42	536.2	79.6	2329	10	ADG05460	ADG05460 Human PRO
43	536.2	79.6	2329	10	ADG82461	ADG82461 Human PRO
44	536.2	79.6	2329	12	ADE51714	ADE51714 Human CDN
45	536.2	79.6	2329	12	ADE51830	ADE51830 Human CDN

ALIGNMENTS

RESULT 1

AAA29059

ID AAA29059 standard; CDNA; 674 BP.

XX AAA29059;

AC AAA29059;

DT 12-SEP-2000 (first entry)

XX Rat TGF-beta binding protein (BEER) CDNA.

XX osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
KW BEER; gene therapy; antisense therapy; fracture; bone mineralization; ss.
XX Rattus norvegicus.

OS Rattus norvegicus.

XX Key Location/Qualifiers

FT CDS 33..674

FT /*tag= a

FT /product= "TGF-beta_binding_protein"

XX WO200032773-A1.

XX 08-JUN-2000.

XX 24-NOV-1999; 99WO-US027990.

XX 27-NOV-1998; 98US-0110283P.

XX (DARW-) DARWIN DISCOVERY LTD.

XX Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;

XX Van Ness J, Winkler DG;

XX WPI; 2000-412321/35.

XX P-PSDB; AAY96433.

XX Nucleic acids (I) encoding a transforming growth factor beta binding
PT protein, useful for identifying agents for treating osteopenia,
PT osteoporosis and fractures.

XX Claim 1; Page 125; 162pp; English.

XX This CDNA encodes a rat transforming growth factor-beta (TGF-beta)

Sequence 13, Appl
Sequence 7, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl

Sequence 13, Appl
Sequence 7, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:55:24 ; Search time 2921.55 Seconds
(without alignments)

9417.841 Million cell updates/sec

Title: US-10-788-606-13

Perfect score: 674

Sequence: 1 gaggaccgagtccttctct.....agctggagacgcctactag 674

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents NA Main:

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- 56: /cgn2_6/ptodata/1/pna/US105A COMB.seq.*
- 57: /cgn2_6/ptodata/1/pna/US105B COMB.seq.*
- 58: /cgn2_6/ptodata/1/pna/US106A COMB.seq.*
- 59: /cgn2_6/ptodata/1/pna/US107A COMB.seq.*
- 60: /cgn2_6/ptodata/1/pna/US107B COMB.seq.*
- 61: /cgn2_6/ptodata/1/pna/US107C COMB.seq.*
- 62: /cgn2_6/ptodata/1/pna/US107D COMB.seq.*
- 63: /cgn2_6/ptodata/1/pna/US108A COMB.seq.*
- 64: /cgn2_6/ptodata/1/pna/US108B COMB.seq.*
- 65: /cgn2_6/ptodata/1/pna/US109A COMB.seq.*
- 66: /cgn2_6/ptodata/1/pna/US109B COMB.seq.*
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- 68: /cgn2_6/ptodata/1/pna/US110 COMB.seq.*
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- 85: /cgn2_6/ptodata/1/pna/US6016 COMB.seq.*
- 86: /cgn2_6/ptodata/1/pna/US6017 COMB.seq.*
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- 105: /cgn2_6/ptodata/1/pna/US6035 COMB.seq.*
- 106: /cgn2_6/ptodata/1/pna/US6036 COMB.seq.*
- 107: /cgn2_6/ptodata/1/pna/US6037 COMB.seq.*
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- 113: /cgn2_6/ptodata/1/pna/US6043 COMB.seq.*
- 114: /cgn2_6/ptodata/1/pna/US6044 COMB.seq.*
- 115: /cgn2_6/ptodata/1/pna/US6045 COMB.seq.*
- 116: /cgn2_6/ptodata/1/pna/US6046 COMB.seq.*

Result No.	Score	Query Match	Length	DB	ID	Description	
1	674	100.0	674	3	US-09-449-218D-13	Sequence 13, Appl	
2	674	100.0	674	4	US-09-668-529A-13	Sequence 13, Appl	
3	674	100.0	674	4	US-09-668-037A-13	Sequence 13, Appl	
4	674	100.0	674	4	US-09-668-021-13	Sequence 13, Appl	
5	556	82.5	638	3	US-09-449-218D-11	Sequence 11, Appl	
6	556	82.5	638	4	US-09-668-529A-11	Sequence 11, Appl	
7	556	82.5	638	4	US-09-668-037A-11	Sequence 11, Appl	
8	556	82.5	638	4	US-09-668-021-11	Sequence 11, Appl	
9	536.2	79.6	2301	3	US-09-449-218D-1	Sequence 1, Appl	
10	536.2	79.6	2301	4	US-09-668-529A-1	Sequence 1, Appl	
11	536.2	79.6	2301	4	US-09-668-037A-1	Sequence 1, Appl	
12	536.2	79.6	2301	4	US-09-668-021-1	Sequence 1, Appl	
13	534.6	79.3	2301	3	US-09-449-218D-3	Sequence 3, Appl	
14	534.6	79.3	2301	3	US-09-449-218D-7	Sequence 7, Appl	
15	534.6	79.3	2301	4	US-09-668-529A-3	Sequence 3, Appl	
16	534.6	79.3	2301	4	US-09-668-529A-7	Sequence 7, Appl	
17	534.6	79.3	2301	4	US-09-668-037A-3	Sequence 3, Appl	
18	534.6	79.3	2301	4	US-09-668-037A-7	Sequence 7, Appl	
19	534.6	79.3	2301	4	US-09-668-021-3	Sequence 3, Appl	
20	534.6	79.3	2301	4	US-09-668-021-7	Sequence 7, Appl	
21	533	79.1	2301	3	US-09-449-218D-5	Sequence 5, Appl	
22	533	79.1	2301	4	US-09-668-529A-5	Sequence 5, Appl	
23	533	79.1	2301	4	US-09-668-037A-5	Sequence 5, Appl	
24	533	79.1	2301	4	US-09-668-021-5	Sequence 5, Appl	
25	530	78.6	642	3	US-09-449-218D-9	Sequence 9, Appl	
26	530	78.6	642	4	US-09-668-529A-9	Sequence 9, Appl	
27	530	78.6	642	4	US-09-668-037A-9	Sequence 9, Appl	

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42 ; Search time 2399.78 Seconds
(without alignments)
10741.894 Million cell updates/sec

Title: US-10-788-606-15
Perfect score: 532
Sequence: 1 agaatgagccacagaatc.....accaaagccagccggccga 532

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pi.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	532	100.0	532	4	AF326738 Bos tauri
2	532	100.0	532	6	BD251913 Compositi
3	532	100.0	532	6	AR258999 Sequence
4	532	100.0	532	6	AR267472 Sequence
5	532	100.0	532	6	AR371672 Sequence
6	467.8	87.9	642	6	AR259025 Sequence
7	467.8	87.9	642	6	AR267498 Sequence
8	467.8	87.9	642	6	AR371698 Sequence
9	467.8	87.9	759	6	AX323453 Sequence
10	467.8	87.9	2271	6	AX342535 Sequence
11	467.8	87.9	2296	9	AF331844 Homo sapi
12	467.8	87.9	2301	6	BD251906 Compositi
13	467.8	87.9	2301	6	BD251907 Compositi
14	467.8	87.9	2301	6	AR258992 Sequence
15	467.8	87.9	2301	6	AR258993 Sequence
16	467.8	87.9	2301	6	AR267465 Sequence
17	467.8	87.9	2301	6	AR267466 Sequence
18	467.8	87.9	2301	6	AR371665 Sequence
19	467.8	87.9	2301	6	AR371666 Sequence

20	467.8	87.9	2323	9	AF326739	AF326739 Homo sapi
21	467.8	87.9	2329	6	AX056687	AX056687 Sequence
22	467.8	87.9	2329	6	AX574536	AX574536 Sequence
23	467.8	87.9	2329	9	AY358627	AY358627 Homo sapi
24	466.2	87.6	2301	6	BD251908	BD251908 Compositi
25	466.2	87.6	2301	6	BD251909	BD251909 Compositi
26	466.2	87.6	2301	6	AR258994	AR258994 Sequence
27	466.2	87.6	2301	6	AR258995	AR258995 Sequence
28	466.2	87.6	2301	6	AR267467	AR267467 Sequence
29	466.2	87.6	2301	6	AR267468	AR267468 Sequence
30	466.2	87.6	2301	6	AR371667	AR371667 Sequence
31	466.2	87.6	2301	6	AR371668	AR371668 Sequence
32	461.4	86.7	642	6	BD251910	BD251910 Compositi
33	461.4	86.7	642	6	AR258996	AR258996 Sequence
34	461.4	86.7	642	6	AR267469	AR267469 Sequence
35	461.4	86.7	642	6	AR371669	AR371669 Sequence
36	461.4	86.7	642	9	AF326742	AF326742 Cercopith
37	424.6	79.8	674	6	BD251912	BD251912 Compositi
38	424.6	79.8	674	6	AR258998	AR258998 Sequence
39	424.6	79.8	674	6	AR267471	AR267471 Sequence
40	424.6	79.8	674	6	AR371671	AR371671 Sequence
41	424.6	79.8	674	10	AF326741	AF326741 Rattus no
42	423.4	79.6	1154	9	AY358203	AY358203 Homo sapi
43	415.8	78.2	636	6	AX323455	AX323455 Sequence
44	414.2	77.9	638	6	BD251911	BD251911 Compositi
45	414.2	77.9	638	6	AR258997	AR258997 Sequence

ALIGNMENTS

RESULT 1	AF326738	Bos taurus	532 bp	mRNA	linear	MAM 28-FEB-2001
LOCUS	AF326738	Bos taurus	sclerostin mRNA, partial cds.			
DEFINITION	AF326738					
ACCESSION	AF326738.1	GI:13161016				
VERSION						
KEYWORDS						
SOURCE		Bos taurus (cow)				
ORGANISM		Bos taurus				
REFERENCE						
AUTHORS						
		Brunkow, M.E., Gardner, J.C., Van Ness, J., Paepker, B.W., Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J., Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P., Galas, D., Hamersma, H., Beighton, P. and Mulligan, J.T.				
TITLE		Bone dysplasia sclerosteosis results from loss of the SOST gene product, a novel cysteine knot-containing protein				
JOURNAL		Am. J. Hum. Genet. 68 (3), 577-589 (2001)				
MEDLINE		21090529				
PUBMED		11179006				
AUTHORS						
		Brunkow, M.E., Gardner, J.C., Van Ness, J., Paepker, B.W., Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J., Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P., Galas, D., Hamersma, H., Beighton, P. and Mulligan, J.T.				
TITLE		Direct Submission				
JOURNAL		Submitted (07-DEC-2000) Genomics, Celltech Chiroscience Inc., 1631 220th St. SE, Bothell, WA 98021, USA				
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:05:42 ; Search time 1956.65 Seconds
(without alignments)

10349.440 Million cell updates/sec

Title: US-10-788-606-15

Perfect score: 532

Sequence: 1 agaatgagccacagaaatc.....acaaagccagcggcgga 532

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467.8	87.9	642	9 AY400962	AY400962 Homo sapi
2	415.8	78.2	636	9 AY400964	AY400964 Mus muscu
3	415.8	78.2	1990	3 AK017295	AK017295 Mus muscu
4	406.4	76.4	667	2 BB636457	BB636457 BB636457
5	394.8	74.2	947	6 BY17106	BY17106 BY17106
6	391.4	73.6	623	2 BB637315	BB637315 BB637315
7	390.2	73.3	637	9 AY400963	AY400963 Pan trogl
C 8	355.8	66.9	419	2 BE101082	BE101082 UI-R-Bu1
9	346.8	65.2	1177	3 AF184211	AF184211 Homo sapi
10	333.4	62.7	494	5 BX282099	BX282099 BX282099
C 11	306.2	57.6	360	1 AI556282	AI556282 UI-R-C2P-
12	293.8	55.2	511	2 BB638050	BB638050 BB638050
C 13	263.8	49.6	315	1 AI113131	AI113131 UI-R-C2P-
C 14	251.4	47.2	291	2 BE111224	BE111224 UI-R-Bu1
15	159.4	30.0	532	1 AL922835	AL922835 AL922835
16	158.4	29.8	716	4 BJ712074	BJ712074 BJ712074
17	148.4	27.9	749	6 CA374043	CA374043 648343 NC
18	140.2	26.4	1880	3 CR681743	CR681743 Tetraodon
19	121.4	22.8	609	9 CR261683	CR261683 Reverse s
C 20	98.4	18.5	535	8 AQ171546	AQ171546 HS 3088 B
21	95.2	17.9	669	2 BF607657	BF607657 MY1 00059
22	93	17.5	575	7 CK625985	CK625985 mj16902.y
23	93	17.5	621	7 CK626761	CK626761 mj25h07.y
24	93	17.5	854	6 BY707967	BY707967 BY707967

25	93	17.5	979	6 BY702931	BY702931 BY702931
26	93	17.5	988	6 BY702775	BY702775 BY702775
27	93	17.5	995	6 BY707897	BY707897 BY707897
28	93	17.5	1612	3 AK002396	AK002396 Mus muscu
29	93	17.5	1613	3 AK007893	AK007893 Mus muscu
30	93	17.5	1690	3 AK002240	AK002240 Mus muscu
31	93	17.5	1691	3 AK007967	AK007967 Mus muscu
32	91.4	17.2	584	7 CF169948	CF169948 B0820807-
33	91.4	17.2	607	7 CF951492	CF951492 UI-M-HL0-
34	89.8	16.9	623	4 BI143761	BI143761 602907224
35	87.8	16.5	619	6 CB579051	CB579051 AMGNNUC:N
36	87.8	16.5	787	7 CO382488	CO382488 AGENCOURT
37	87.8	16.5	823	7 CK602002	CK602002 AGENCOURT
38	85.2	16.0	789	3 AK007935	AK007935 Mus muscu
C 39	84.2	15.8	799	6 CD742451	CD742451 UI-M-AQ0-
40	83.6	15.7	671	6 CB841630	CB841630 M15E-2194
41	83.4	15.7	710	5 BX266741	BX266741 BX266741
42	83	15.6	355	1 AA197904	AA197904 mv05C05.f
43	83	15.6	433	1 AA067619	AA067619 mm23e07.f
44	82.2	15.5	723	4 BJ731200	BJ731200 BJ731200
45	82	15.4	746	7 CK473258	CK473258 AGENCOURT

ALIGNMENTS

RESULT 1
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LOCUS: AY400962 Homo sapiens SOST gene, VIRTUAL TRANSCRIPT, partial sequence, 642 bp DNA linear GSS 15-DEC-2003
DEFINITION: Homo sapiens SOST gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION: AY400962 GI:39756951
VERSION: AY400962.1
KEYWORDS: GSS.
SOURCE: Homo sapiens (human)
ORGANISM: Homo sapiens
REFERENCE: 1 (bases 1 to 642)
AUTHORS: Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferrier, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE: Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL: Science 302 (5652), 1960-1963 (2003)
PUBMED: 14671302
REFERENCE: 2 (bases 1 to 642)
AUTHORS: Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferrier, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE: Direct Submission
JOURNAL: Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT: This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES: Location/Qualifiers
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gene: <1..>642
/genes="SOST"
ORIGIN: /locus_tag="HOM0732"
Query Match 87.9%; Score 467.8; DB 9; Length 642;
Best Local Similarity 93.5%; Pred. No. 1.6e-90;
Matches 500; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
QY 1 AGAATGATGCACAGAAATCATCCCGAGTGGCGAGTACCCGAGCTTCGACAGC 60
|||||

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:54:42 ; Search time 309.833 Seconds
(without alignments)
10164.517 Million cell updates/sec

Title: US-10-788-606-15

Perfect score: 532

Sequence: 1 agaatgatgccacagaatc.....accaaagccagccggcgca 532

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	532	100.0	532	3	AAA29060 Bovine TG
2	532	100.0	532	12	ADI27209 Cow LRP b
3	532	100.0	532	13	ADSI12972 TGF-beta
4	467.8	87.9	642	3	AAA94051 Human DAN
5	467.8	87.9	642	12	ADI27109 Human LRP
6	467.8	87.9	759	6	ABA94293 Human cto
7	467.8	87.9	2271	6	AAI27576 Human ost
8	467.8	87.9	2301	3	AAA29061 Mutant hu
9	467.8	87.9	2301	3	AAA29055 Human TGF
10	467.8	87.9	2301	13	ADSI12960 TGF-beta
11	467.8	87.9	2301	13	ADSI12958 TGF-beta
12	467.8	87.9	2323	10	ACF79824 Human SOS
13	467.8	87.9	2329	4	AAA91023 Human sec
14	467.8	87.9	2329	6	ABK69992 cDNA enco
15	467.8	87.9	2329	9	ADA01331 Human PRO
16	467.8	87.9	2329	9	ADA43760 Human CDN
17	467.8	87.9	2329	9	ADA43528 Human CDN
18	467.8	87.9	2329	9	ADA01203 Human PRO
19	467.8	87.9	2329	9	ADA01087 Human CDN
20	467.8	87.9	2329	9	ADA43644 Human CDN

21	467.8	87.9	2329	9	ADA06906	Ada06906 Human PRO
22	467.8	87.9	2329	9	ADA08394	Ada08394 Novel hum
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24	467.8	87.9	2329	9	ADB86970	ADB86970 Human PRO
25	467.8	87.9	2329	9	ADB66125	ADB66125 Human CDN
26	467.8	87.9	2329	10	ADB99803	ADB99803 Human PRO
27	467.8	87.9	2329	10	ADB99458	ADB99458 Novel hum
28	467.8	87.9	2329	10	ADB66009	ADB66009 Human CDN
29	467.8	87.9	2329	10	ADC23407	ADC23407 Human CDN
30	467.8	87.9	2329	10	ADC26100	ADC26100 Human PRO
31	467.8	87.9	2329	10	ADE04927	ADE04927 Human PRO
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33	467.8	87.9	2329	10	ADD88164	ADD88164 Human PRO
34	467.8	87.9	2329	10	ADD95459	ADD95459 Human CDN
35	467.8	87.9	2329	10	ADE06389	ADE06389 Human PRO
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43	467.8	87.9	2329	12	ADE51714	ADE51714 Human CDN
44	467.8	87.9	2329	12	ADE51830	ADE51830 Human CDN
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ALIGNMENTS

RESULT 1

AAA29060
ID AAA29060 standard; cDNA; 532 BP.

XX
AC AAA29060;

DT 12-SEP-2000 (first entry)

DE Bovine TGF-beta binding protein (BEER) cDNA.

XX osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
KW BEER; gene therapy; antisense therapy; fracture; bone mineralization; ss.

OS Bos taurus.

XX Key Location/Qualifiers

FT CDS 1..530

FT /*tag= a

FT /partial

FT /product= "TGF-beta_binding_protein"

XX WO200032773-A1.

PD 08-JUN-2000.

XX 24-NOV-1999; 99WO-US027990.

XX 27-NOV-1998; 98US-0110283P.

XX (DARW-) DARWIN DISCOVERY LTD.

XX Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepker BW;

XX Van Ness J, Winkler DG;

XX WPI; 2000-412321/35.

XX P-PSDB; AAY96434.

XX Nucleic acids (I) encoding a transforming growth factor beta binding
FT protein, useful for identifying agents for treating osteopenia,
FT osteoporosis and fractures.

XX Claim 1; Page 126; 162pp; English.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 15:15:06 ; Search time 355.843 Seconds
(without alignments)
9344.794 Million cell updates/sec

Title: US-10-788-606-15

Perfect score: 532

Sequence: 1 agaatgaccagaaatc.....accagcgccggcgca 532

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6067389 seqs, 312528755 residues

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	532	100.0	532	16	US-10-384-893-15
2	532	100.0	532	17	US-10-463-190-15
3	532	100.0	532	17	US-10-463-190-15
4	532	100.0	532	18	US-10-464-368-110
5	532	100.0	532	18	US-10-095-248A-15
6	532	100.0	532	19	US-10-788-606-15
7	532	100.0	532	21	US-10-799-162-15
7	532	100.0	532	21	US-10-868-497-69

8	467.8	87.9	570	17	US-10-463-190-100	Sequence 100, Appl
9	467.8	87.9	570	21	US-10-868-497-55	Sequence 55, Appl
10	467.8	87.9	570	21	US-10-384-893-45	Sequence 45, Appl
11	467.8	87.9	570	21	US-10-463-190-45	Sequence 45, Appl
12	467.8	87.9	570	21	US-10-464-368-10	Sequence 10, Appl
13	467.8	87.9	570	21	US-10-095-248A-45	Sequence 45, Appl
14	467.8	87.9	570	21	US-09-867-274-1	Sequence 1, Appl
15	467.8	87.9	570	21	US-10-311-490A-1	Sequence 1, Appl
16	467.8	87.9	570	21	US-10-384-893-1	Sequence 1, Appl
17	467.8	87.9	570	21	US-10-384-893-3	Sequence 3, Appl
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44	467.8	87.9	570	21	US-10-246-210-63	Sequence 63, Appl
45	467.8	87.9	570	21	US-10-239-196-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1

US-10-384-893-15

; Sequence 15, Application US/10384893

; Publication No. US20030166247A1

; GENERAL INFORMATION:

; APPLICANT: Brunkow, Mary E.

; APPLICANT: Galas, David J.

; APPLICANT: Kovacevich, Brian

; APPLICANT: Mulligan, John T.

; APPLICANT: Paepers, Bryan W.

; APPLICANT: Van Nessel, Jeffrey

; APPLICANT: Winkler, David G.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING

; FILE OF INVENTION: BONE MINERALIZATION

; FILE REFERENCE: 240083.508D5

; CURRENT APPLICATION NUMBER: US/10/384,893

; CURRENT FILING DATE: 2003-03-06

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 15

; LENGTH: 532

; TYPE: DNA

; ORGANISM: Bos torus

; US-10-384-893-15

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Best Local Similarity 100.0%; Pred. No. 8.4e-134;

Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAATGATGCCAGAAATCATCCCGAGTGGCGGAGTACCCGAGCCTCTGCCAGAC 60

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:55:24 ; Search time 2306.03 Seconds
(without alignments)
9417.841 Million cell updates/sec

Title: US-10-788-606-15

Perfect score: 532

Sequence: 1 agaatgatccacagaatc.....accaaagccagccggcgca 532

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:55:24 ; Search time 374.306 Seconds
(without alignments)
6348.430 Million cell updates/sec

Title: US-10-788-606-15

Perfect score: 532

Sequence: .1 agaatgagccacagaaatc.....acaaagccagcgccgga 532

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 13027057 seqs, 2233325459 residues

Total number of hits satisfying chosen parameters: 26054114

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /cgn2_6/prodata/2/pna/US11_NEW_COMB.seq2.*
14: /cgn2_6/prodata/2/pna/US11_NEW_COMB.seq3.*
15: /cgn2_6/prodata/2/pna/US11_NEW_COMB.seq4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467.8	87.9	570	15	US-60-677-583-99
2	467.8	87.9	2302	15	US-60-680-544-44583
3	467.8	87.9	2302	15	US-60-680-473-44583
4	76.4	14.4	1089	15	US-60-680-544-23752
5	76.4	14.4	1089	15	US-60-680-473-23752
6	72.2	13.6	2337	1	PCT-US05-13260-1
7	54	10.2	927	13	US-11-031-175-9087
8	54	10.2	11963	13	US-11-031-175-1072
9	53	10.0	945	13	US-11-031-175-7231
10	53	10.0	4486	13	US-11-031-175-677
11	52	9.8	880	15	US-60-680-544-48429
12	52	9.8	880	15	US-60-680-473-48429
13	51.8	9.7	1103	15	US-60-669-175-7216
14	50.4	9.5	1216	15	US-60-669-241-24312
15	49.6	9.3	28493	9	US-11-031-175-1241
16	49.2	9.2	1917	9	US-10-703-032-28735
17	48.4	9.1	8563	13	US-11-031-175-3318
18	48.4	9.1	10178	13	US-11-031-175-977

C 19	48.4	9.1	11805	13	US-11-031-175-1016	Sequence 1016, Ap
C 20	48.4	9.1	15251	13	US-11-031-175-1154	Sequence 1154, Ap
C 21	48.2	9.1	593	9	US-10-703-032-54375	Sequence 54375, A
C 22	48.2	9.1	7850	13	US-11-031-175-749	Sequence 749, App
C 23	47.8	9.0	591	13	US-11-031-175-4897	Sequence 4897, Ap
C 24	47.8	9.0	3839	12	US-11-090-997-1471	Sequence 1471, Ap
C 25	47.6	8.9	1437	13	US-11-031-175-4786	Sequence 4786, Ap
C 26	47.6	8.9	27903	13	US-11-031-175-1235	Sequence 1235, Ap
C 27	47.4	8.9	552	9	US-10-703-032-10967	Sequence 10967, A
C 28	47.4	8.9	152132	11	US-10-940-774A-13845	Sequence 13845, A
C 29	47.4	8.9	152145	11	US-10-940-774A-12371	Sequence 12371, A
C 30	47.2	8.9	969	13	US-11-053-052-18	Sequence 18, Appl
C 31	47.2	8.9	969	13	US-11-053-576-18	Sequence 18, Appl
C 32	47.2	8.9	2016	2	PCT-US05-06729-27	Sequence 27, Appl
C 33	47.2	8.9	4830849	2	PCT-IB03-06509-1355	Sequence 1355, Ap
C 34	47	8.8	779	9	US-10-703-032-31002	Sequence 31002, A
C 35	47	8.8	1271	9	US-10-703-032-3621	Sequence 3621, Ap
C 36	47	8.8	1587	1	PCT-US05-10257-137	Sequence 137, App
C 37	46.8	8.8	553	9	US-10-703-032-16224	Sequence 16224, A
C 38	46.8	8.8	8610	1	PCT-US05-13243-6	Sequence 6, Appli
C 39	46.8	8.8	8610	12	US-11-109-593-6	Sequence 6, Appli
C 40	46.8	8.8	67323	1	PCT-US05-13243-1	Sequence 1, Appli
C 41	46.8	8.8	67323	12	US-11-109-593-1	Sequence 1, Appli
C 42	46.8	8.8	4830849	2	PCT-IB03-06509-1355	Sequence 1355, Ap
C 43	46.6	8.8	620	9	US-10-703-032-74411	Sequence 74411, A
C 44	46.6	8.8	584	9	US-10-703-032-35211	Sequence 35211, A
C 45	46.4	8.7	1216	15	US-60-669-241-24312	Sequence 24312, A

ALIGNMENTS

RESULT 1

US-60-677-583-99
; Sequence 99, Application US/60677583
; GENERAL INFORMATION:
; APPLICANT: Lu, Heieng Sen
; APPLICANT: Fastcy, Chris
; APPLICANT: Robinson, Martyn
; APPLICANT: Stephens, Paul Edward
; APPLICANT: Kirby, Hishani
; APPLICANT: Henry, Alistair James
; APPLICANT: Latham, John
; APPLICANT: Ramsdell, Fred
; APPLICANT: Winkler, David
; TITLE OF INVENTION: EPITOPES
; FILE REFERENCE: 60117-163
; CURRENT APPLICATION NUMBER: US/60/677,583
; CURRENT FILING DATE: 2005-05-03
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-677-583-99

Query Match 87.9%; Score 467.8; DB 15; Length 570;

Best Local Similarity 93.5%; Pred. No. 5.7e-70;

Mismatches 500; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

QY 1 AGAATGATGCCACAGAAATCATCCCGAGCTGGCGAGTACCCCGAGCTTCCCGAGCAGC 60

DB 20 AGAATGATGCCACGGAATCATCCCGAGCTGGCGAGTACCCCGAGCTTCCCGAGCAGC 79

QY 61 T---GACACACAGACCATGACCGCGGAGACCGAGGAGCTCCCGAGCAGCCTCCCGAGCAGCCT 117

DB 80 TGGAGAACCAACAGACCATGACCGCGGAGACCGAGGAGCTCCCGAGCAGCCTCCCGAGCAGCCT 139

QY 118 TTGAGACCAACAGACCGCTCCGAGTACAGCTGCGGAGCTGCACCTTCCCGAGCAGCCTTCCCGAGCAGCCT 177

DB 140 TTGAGACCAACAGACCGCTCCGAGTACAGCTGCGGAGCTGCACCTTCCCGAGCAGCCTTCCCGAGCAGCCT 199

